

Combined functional profiling of dermatitis and psoriasis datasets using GO Biological Process

465 significant modules

LOR indicates Log Odds Ratio of the coefficient or the interaction

p indicates FDR adjusted p-value

	LOR t d	LOR t p	LOR In-ter	p t d	p t p	p Inter	pattern	name
GO:0022403	-0.13	0.36	0.11	0.11	0.00	0.01	q1i	cell cycle phase
GO:0000279	-0.06	0.37	0.12	0.55	0.00	0.03	q1i	M phase
GO:0051301	-0.10	0.25	0.15	0.36	0.00	0.00	q1i	cell division
GO:0000087	-0.11	0.40	0.12	0.32	0.00	0.05	q1i	M phase of mitotic cell cycle
GO:0048015	0.08	0.07	0.16	0.72	0.68	0.05	b13	phosphoinositide-mediated signaling
GO:0000302	0.24	-0.06	0.29	0.59	0.85	0.00	b13	response to reactive oxygen species
GO:0032945	0.43	0.33	-0.79	0.26	0.39	0.00	b24	negative regulation of mononuclear cell proliferation
GO:0050672	0.43	0.33	-0.79	0.26	0.39	0.00	b24	negative regulation of lymphocyte proliferation
GO:0048589	-0.19	-0.06	-0.59	0.53	0.91	0.04	b24	developmental growth
GO:0007028	0.21	-0.11	-0.75	0.47	0.83	0.00	b24	cytoplasm organization and biogenesis
GO:0007043	0.07	-0.50	-0.91	0.86	0.22	0.00	b24	cell-cell junction assembly
GO:0045216	0.12	-0.26	-0.86	0.75	0.59	0.00	b24	cell-cell junction assembly and maintenance
GO:0009607	0.35	0.19	0.05	0.00	0.02	0.69	q1f	response to biotic stimulus
GO:0051704	0.31	0.16	0.05	0.00	0.03	0.68	q1f	multi-organism process
GO:0045893	-0.23	0.24	-0.05	0.00	0.00	0.78	q2f	positive regulation of transcription, DNA-dependent
GO:0045935	-0.19	0.23	-0.05	0.01	0.00	0.72	q2f	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0045941	-0.22	0.23	-0.05	0.00	0.00	0.78	q2f	positive regulation of transcription
GO:0051254	-0.23	0.24	-0.05	0.00	0.00	0.78	q2f	positive regulation of RNA metabolic process
GO:0016481	-0.36	0.18	0.05	0.00	0.02	0.61	q2f	negative regulation of transcription
GO:0045892	-0.31	0.21	0.01	0.00	0.02	0.99	q2f	negative regulation of transcription, DNA-dependent
GO:0045934	-0.36	0.19	0.04	0.00	0.01	0.75	q2f	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0051253	-0.33	0.22	0.00	0.00	0.01	0.99	q2f	negative regulation of RNA metabolic process
GO:0009719	-0.20	0.30	0.04	0.00	0.00	0.73	q2f	response to endogenous stimulus
GO:0006281	-0.23	0.19	-0.01	0.01	0.03	0.99	q2f	DNA repair
GO:0006974	-0.22	0.29	0.05	0.00	0.00	0.68	q2f	response to DNA damage stimulus
GO:0006512	-0.42	0.16	-0.01	0.00	0.03	0.95	q2f	
GO:0016567	-0.41	0.36	-0.04	0.00	0.01	0.93	q2f	protein ubiquitination
GO:0032446	-0.38	0.29	-0.03	0.00	0.05	0.94	q2f	protein modification by small protein conjugation
GO:0016125	-0.34	0.31	-0.05	0.02	0.03	0.87	q2f	sterol metabolic process
GO:0006913	-0.28	0.43	-0.07	0.00	0.00	0.71	q2f	nucleocytoplasmic transport
GO:0051169	-0.28	0.43	-0.07	0.00	0.00	0.71	q2f	nuclear transport
GO:0006605	-0.23	0.35	-0.01	0.01	0.00	0.97	q2f	protein targeting
GO:0006606	-0.27	0.39	-0.03	0.05	0.00	0.94	q2f	protein import into nucleus
GO:0006886	-0.18	0.27	0.00	0.00	0.00	0.99	q2f	intracellular protein transport
GO:0043285	-0.18	0.18	0.02	0.02	0.03	0.93	q2f	biopolymer catabolic process
GO:0008544	-0.29	0.40	0.12	0.01	0.00	0.13	q2f	epidermis development
GO:0030163	-0.23	0.20	0.02	0.01	0.04	0.94	q2f	protein catabolic process
GO:0016071	-0.32	0.27	-0.09	0.00	0.00	0.48	q2f	mRNA metabolic process
GO:0008380	-0.37	0.34	-0.11	0.00	0.00	0.47	q2f	RNA splicing
GO:0006397	-0.34	0.32	-0.11	0.00	0.00	0.39	q2f	mRNA processing
GO:0006403	-0.34	0.35	-0.06	0.03	0.02	0.85	q2f	RNA localization
GO:0015931	-0.39	0.40	-0.04	0.01	0.00	0.93	q2f	nucleobase, nucleoside, nucleotide and nucleic acid transport
GO:0050657	-0.36	0.38	-0.05	0.02	0.01	0.90	q2f	nucleic acid transport
GO:0051236	-0.36	0.38	-0.05	0.02	0.01	0.90	q2f	establishment of RNA localization
GO:0050658	-0.36	0.38	-0.05	0.02	0.01	0.90	q2f	RNA transport
GO:0051028	-0.39	0.34	-0.04	0.02	0.04	0.94	q2f	mRNA transport
GO:0022613	-0.31	0.39	0.00	0.00	0.00	0.99	q2f	ribonucleoprotein complex biogenesis and assembly
GO:0006413	-0.50	0.39	0.05	0.00	0.00	0.81	q2f	translational initiation
GO:0022618	-0.48	0.40	-0.02	0.00	0.00	0.95	q2f	ribonucleoprotein complex assembly
GO:0000082	-0.51	0.47	0.07	0.02	0.02	0.82	q2f	G1/S transition of mitotic cell cycle
GO:0006888	-0.46	0.41	0.03	0.00	0.00	0.92	q2f	ER to Golgi vesicle-mediated transport
GO:0040029	-0.44	0.39	0.01	0.01	0.02	0.99	q2f	regulation of gene expression, epigenetic
GO:0000075	-0.40	0.63	0.01	0.00	0.00	0.98	q2f	cell cycle checkpoint
GO:0007093	-0.43	0.57	0.05	0.02	0.00	0.87	q2f	mitotic cell cycle checkpoint
GO:0006470	-0.24	0.25	-0.10	0.03	0.03	0.65	q2f	protein amino acid dephosphorylation
GO:0007567	-0.80	0.64	0.04	0.01	0.02	0.95	q2f	parturition
GO:0044257	-0.39	0.30	0.05	0.00	0.00	0.80	q2f	cellular protein catabolic process
GO:0006511	-0.40	0.29	0.05	0.00	0.00	0.80	q2f	ubiquitin-dependent protein catabolic process
GO:0019941	-0.39	0.30	0.05	0.00	0.00	0.78	q2f	modification-dependent protein catabolic process
GO:0043632	-0.39	0.30	0.05	0.00	0.00	0.78	q2f	modification-dependent macromolecule catabolic process

GO:0051603	-0.39	0.30	0.05	0.00	0.00	0.79	q2f	proteolysis involved in cellular protein catabolic process
GO:0000375	-0.44	0.36	-0.14	0.00	0.01	0.61	q2f	RNA splicing, via transesterification reactions
GO:0000377	-0.44	0.36	-0.14	0.00	0.01	0.61	q2f	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	-0.44	0.36	-0.14	0.00	0.01	0.61	q2f	nuclear mRNA splicing, via spliceosome
GO:0045646	-0.66	0.81	-0.21	0.05	0.00	0.71	q2f	regulation of erythrocyte differentiation
GO:0030216	-0.48	0.61	0.15	0.02	0.00	0.38	q2f	keratinocyte differentiation
GO:0016573	-0.83	-0.71	-0.60	0.00	0.04	0.08	q3f	histone acetylation
GO:0006892	-0.63	-0.80	-0.56	0.02	0.01	0.13	q3f	post-Golgi vesicle-mediated transport
GO:0015698	0.50	-0.28	-0.27	0.00	0.05	0.22	q4f	inorganic anion transport
GO:0016477	0.26	-0.20	0.08	0.00	0.02	0.52	q4f	cell migration
GO:0051239	0.22	-0.22	-0.03	0.01	0.00	0.87	q4f	regulation of multicellular organismal process
GO:0030182	0.20	-0.34	0.04	0.04	0.00	0.81	q4f	neuron differentiation
GO:0016051	0.33	-0.42	-0.05	0.03	0.00	0.90	q4f	carbohydrate biosynthetic process
GO:0030029	0.25	-0.26	0.09	0.01	0.00	0.47	q4f	actin filament-based process
GO:0030036	0.23	-0.28	0.08	0.02	0.00	0.54	q4f	actin cytoskeleton organization and biogenesis
GO:0016337	0.23	-0.22	0.03	0.02	0.01	0.87	q4f	cell-cell adhesion
GO:0031032	0.73	-0.88	0.10	0.02	0.00	0.84	q4f	actomyosin structure organization and biogenesis
GO:0048627	0.85	-0.80	0.11	0.00	0.00	0.80	q4f	myoblast development
GO:0048628	0.85	-0.80	0.11	0.00	0.00	0.80	q4f	myoblast maturation
GO:0007600	0.18	-0.23	-0.02	0.01	0.00	0.90	q4f	sensory perception
GO:0031589	0.36	-0.29	0.10	0.02	0.05	0.60	q4f	cell-substrate adhesion
GO:0050953	0.23	-0.34	-0.02	0.05	0.00	0.97	q4f	sensory perception of light stimulus
GO:0007601	0.23	-0.34	-0.02	0.05	0.00	0.97	q4f	visual perception
GO:0043062	0.60	-0.62	0.01	0.00	0.00	0.99	q4f	extracellular structure organization and biogenesis
GO:0030198	0.67	-0.69	0.05	0.00	0.00	0.91	q4f	extracellular matrix organization and biogenesis
GO:0051046	0.49	-0.42	0.04	0.03	0.04	0.94	q4f	regulation of secretion
GO:0006817	0.87	-0.61	-0.10	0.00	0.00	0.81	q4f	phosphate transport
GO:0032963	0.94	-0.72	0.07	0.00	0.01	0.93	q4f	collagen metabolic process
GO:0006957	1.12	-0.88	0.17	0.02	0.03	0.79	q4f	complement activation, alternative pathway
GO:0006812	0.16	0.05	-0.09	0.02	0.59	0.47	xh	cation transport
GO:0030001	0.18	-0.02	-0.07	0.02	0.91	0.64	xh	metal ion transport
GO:0019932	0.21	0.04	0.06	0.02	0.77	0.64	xh	second-messenger-mediated signaling
GO:0006820	0.47	-0.16	-0.26	0.00	0.28	0.15	xh	anion transport
GO:0033238	0.44	-0.12	0.14	0.05	0.62	0.54	xh	regulation of amine metabolic process
GO:0001932	0.51	-0.15	0.15	0.02	0.55	0.48	xh	regulation of protein amino acid phosphorylation
GO:0031401	0.58	0.11	0.02	0.04	0.80	0.99	xh	positive regulation of protein modification process
GO:0006521	0.50	-0.15	0.15	0.03	0.56	0.51	xh	regulation of amino acid metabolic process
GO:0033240	0.76	-0.05	0.08	0.01	0.91	0.90	xh	positive regulation of amine metabolic process
GO:0001934	0.77	-0.09	0.09	0.01	0.85	0.86	xh	positive regulation of protein amino acid phosphorylation
GO:0050730	0.53	-0.14	0.15	0.04	0.62	0.60	xh	regulation of peptidyl-tyrosine phosphorylation
GO:0045764	0.77	-0.09	0.09	0.01	0.85	0.86	xh	positive regulation of amino acid metabolic process
GO:0050731	0.91	-0.07	0.07	0.01	0.89	0.93	xh	positive regulation of peptidyl-tyrosine phosphorylation
GO:0002682	0.27	-0.04	-0.11	0.02	0.85	0.66	xh	regulation of immune system process
GO:0002684	0.32	-0.08	-0.05	0.01	0.62	0.90	xh	positive regulation of immune system process
GO:0048583	0.27	-0.01	-0.12	0.03	0.99	0.66	xh	regulation of response to stimulus
GO:0048584	0.37	-0.06	-0.07	0.01	0.79	0.82	xh	positive regulation of response to stimulus
GO:0051240	0.30	-0.13	-0.01	0.01	0.37	0.99	xh	positive regulation of multicellular organismal process
GO:0002694	0.33	0.13	-0.15	0.03	0.51	0.66	xh	regulation of leukocyte activation
GO:0050865	0.33	0.13	-0.15	0.03	0.51	0.66	xh	regulation of cell activation
GO:0051241	0.36	-0.26	-0.09	0.04	0.17	0.82	xh	negative regulation of multicellular organismal process
GO:0051249	0.38	0.15	-0.16	0.01	0.46	0.63	xh	regulation of lymphocyte activation
GO:0050878	0.31	-0.18	0.03	0.02	0.19	0.94	xh	regulation of body fluid levels
GO:0007599	0.32	-0.16	0.02	0.03	0.30	0.95	xh	hemostasis
GO:0009611	0.39	-0.04	0.09	0.00	0.67	0.17	xh	response to wounding
GO:0050817	0.34	-0.17	0.03	0.02	0.30	0.93	xh	coagulation
GO:0006959	0.63	0.03	0.02	0.00	0.86	0.94	xh	humoral immune response
GO:0051707	0.50	0.20	0.03	0.00	0.05	0.90	xh	response to other organism
GO:0007596	0.32	-0.14	0.03	0.03	0.42	0.93	xh	blood coagulation
GO:0019730	0.77	0.16	-0.11	0.00	0.47	0.78	xh	antimicrobial humoral response
GO:0007610	0.28	-0.03	0.08	0.00	0.73	0.32	xh	behavior
GO:0007626	0.33	0.00	0.08	0.00	0.99	0.54	xh	locomotory behavior
GO:0042330	0.46	0.18	0.01	0.00	0.24	0.99	xh	taxis
GO:0002250	0.40	-0.06	-0.03	0.01	0.81	0.95	xh	adaptive immune response
GO:0002252	0.32	0.03	-0.01	0.02	0.87	0.99	xh	immune effector process
GO:0002443	0.39	0.12	-0.08	0.01	0.55	0.82	xh	leukocyte mediated immunity
GO:0002449	0.38	0.07	-0.07	0.02	0.76	0.84	xh	lymphocyte mediated immunity
GO:0002460	0.40	-0.06	-0.03	0.01	0.81	0.95	xh	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0016064	0.53	-0.25	-0.08	0.00	0.27	0.89	xh	immunoglobulin mediated immune response
GO:0019724	0.53	-0.25	-0.08	0.00	0.27	0.89	xh	B cell mediated immunity
GO:0002696	0.46	-0.05	0.04	0.01	0.84	0.94	xh	positive regulation of leukocyte activation
GO:0045191	0.98	-0.22	-0.31	0.00	0.75	0.78	xh	regulation of isotype switching
GO:0045830	1.16	0.18	-0.56	0.00	0.82	0.56	xh	positive regulation of isotype switching
GO:0045911	1.16	0.18	-0.56	0.00	0.82	0.56	xh	positive regulation of DNA recombination
GO:0048291	1.33	0.44	-0.61	0.00	0.62	0.56	xh	isotype switching to IgG isotypes
GO:0048302	1.33	0.44	-0.61	0.00	0.62	0.56	xh	regulation of isotype switching to IgG isotypes
GO:0050867	0.46	-0.05	0.04	0.01	0.84	0.94	xh	positive regulation of cell activation
GO:0051054	0.73	0.50	-0.54	0.02	0.12	0.23	xh	positive regulation of DNA metabolic process
GO:0051251	0.45	-0.02	0.01	0.01	0.92	0.99	xh	positive regulation of lymphocyte activation
GO:0006968	0.47	0.16	-0.10	0.00	0.42	0.78	xh	cellular defense response
GO:0006935	0.46	0.18	0.01	0.00	0.24	0.99	xh	chemotaxis
GO:0006954	0.49	0.00	0.09	0.00	0.99	0.41	xh	inflammatory response
GO:0005996	0.33	0.00	0.05	0.00	1.00	0.81	xh	monosaccharide metabolic process
GO:0044262	0.22	-0.07	0.03	0.00	0.47	0.84	xh	cellular carbohydrate metabolic process
GO:0015980	0.21	-0.07	0.03	0.00	0.43	0.82	xh	energy derivation by oxidation of organic compounds
GO:0019318	0.33	-0.01	0.05	0.00	0.96	0.80	xh	hexose metabolic process
GO:0006006	0.34	-0.02	0.04	0.01	0.91	0.90	xh	glucose metabolic process
GO:0030003	0.22	-0.05	0.02	0.05	0.71	0.93	xh	cellular cation homeostasis
GO:0055065	0.27	-0.08	0.03	0.01	0.53	0.91	xh	metal ion homeostasis
GO:0055080	0.22	-0.09	0.02	0.04	0.47	0.94	xh	cation homeostasis
GO:0006875	0.27	-0.08	0.03	0.01	0.53	0.91	xh	cellular metal ion homeostasis

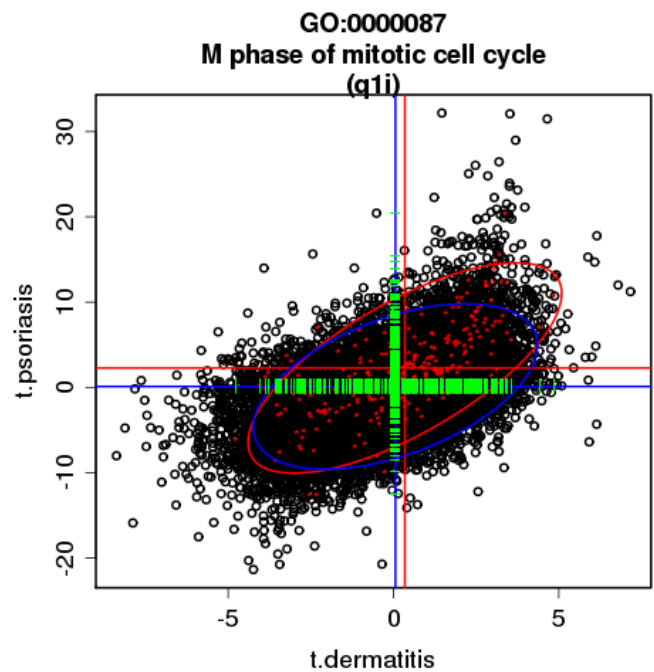
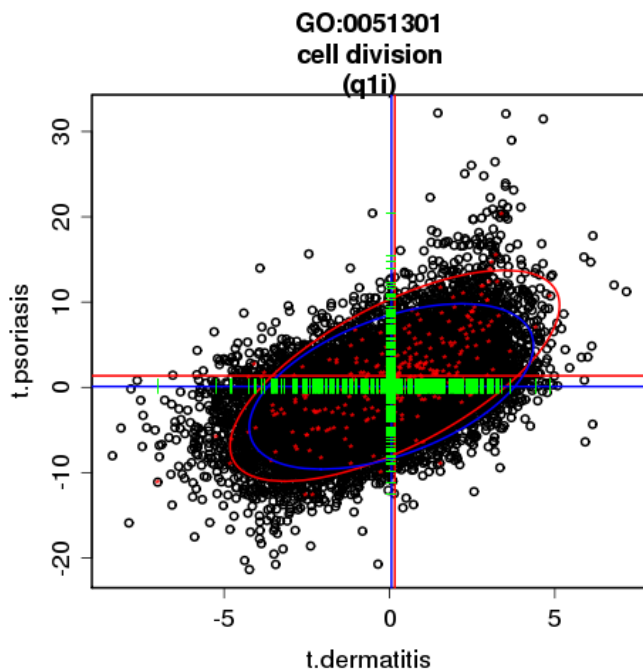
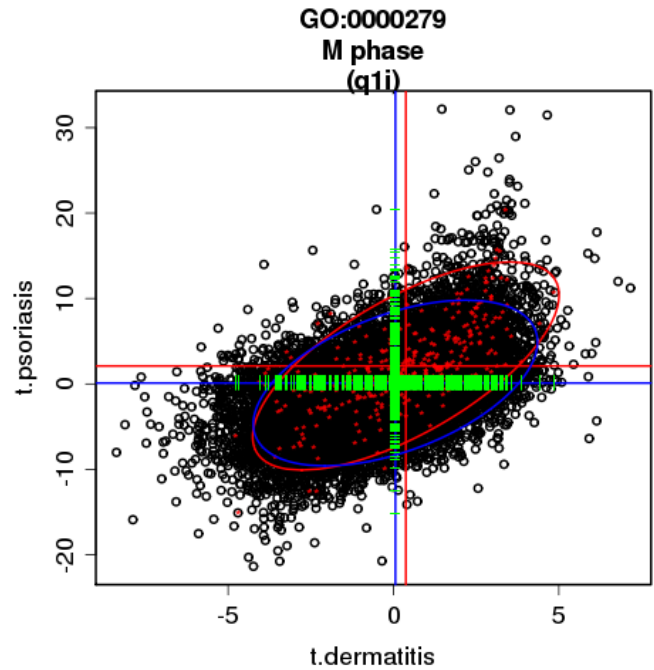
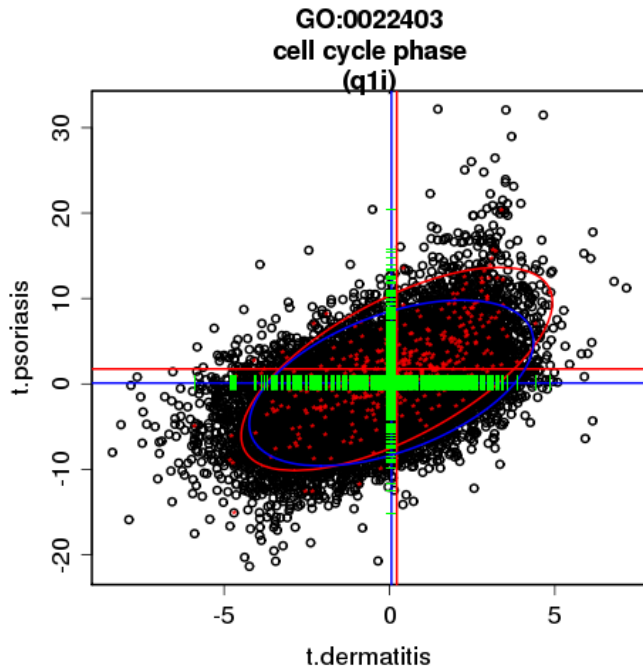
GO:0030005	0.28	-0.08	0.02	0.01	0.59	0.94	xh	cellular di-, tri-valent inorganic cation homeostasis
GO:0055066	0.28	-0.08	0.02	0.01	0.59	0.94	xh	di-, tri-valent inorganic cation homeostasis
GO:0055074	0.29	-0.09	0.03	0.02	0.57	0.90	xh	calcium ion homeostasis
GO:0006874	0.29	-0.09	0.03	0.02	0.57	0.90	xh	cellular calcium ion homeostasis
GO:0045214	1.16	-0.69	-0.11	0.02	0.26	0.95	xh	sarcomere organization
GO:0048646	0.28	-0.00	0.00	0.01	0.97	0.99	xh	anatomical structure formation
GO:0007160	0.35	-0.28	0.11	0.03	0.05	0.56	xh	cell-matrix adhesion
GO:0051480	0.44	-0.08	0.08	0.01	0.73	0.80	xh	cytosolic calcium ion homeostasis
GO:0007204	0.45	-0.04	0.07	0.01	0.85	0.83	xh	elevation of cytosolic calcium ion concentration
GO:0032103	0.73	-0.47	0.08	0.03	0.17	0.90	xh	positive regulation of response to external stimulus
GO:0050920	1.14	0.12	-0.13	0.04	0.91	0.94	xh	regulation of chemotaxis
GO:0006897	0.22	-0.04	-0.04	0.04	0.78	0.87	xh	endocytosis
GO:0010324	0.22	-0.04	-0.04	0.04	0.78	0.87	xh	membrane invagination
GO:0019935	0.32	-0.05	-0.16	0.01	0.83	0.53	xh	cyclic-nucleotide-mediated signaling
GO:0007187	0.38	-0.04	-0.20	0.00	0.85	0.47	xh	G-protein signaling, coupled to cyclic nucleotide second messenger
GO:0007188	0.34	-0.17	-0.18	0.03	0.37	0.60	xh	G-protein signaling, coupled to cAMP nucleotide second messenger
GO:0002526	0.48	-0.32	-0.04	0.01	0.09	0.94	xh	acute inflammatory response
GO:0015672	0.22	0.08	-0.15	0.01	0.48	0.32	xh	monovalent inorganic cation transport
GO:0006813	0.34	-0.08	-0.09	0.01	0.66	0.78	xh	potassium ion transport
GO:0051346	0.83	-0.11	0.23	0.03	0.82	0.47	xh	negative regulation of hydrolase activity
GO:0019882	0.78	0.01	-0.08	0.00	0.97	0.83	xh	antigen processing and presentation
GO:0048002	0.66	0.03	-0.08	0.00	0.91	0.90	xh	antigen processing and presentation of peptide antigen
GO:0002474	0.58	0.03	-0.05	0.01	0.91	0.94	xh	antigen processing and presentation of peptide antigen via MHC class I
GO:0048514	0.23	0.02	0.00	0.04	0.91	1.00	xh	blood vessel morphogenesis
GO:0001654	0.59	0.18	-0.18	0.02	0.60	0.78	xh	eye development
GO:0046530	1.05	0.44	-0.45	0.00	0.42	0.60	xh	photoreceptor cell differentiation
GO:0048592	0.72	0.50	-0.32	0.02	0.16	0.64	xh	eye morphogenesis
GO:0001754	1.08	0.47	-0.46	0.00	0.40	0.59	xh	eye photoreceptor cell differentiation
GO:0042461	1.05	0.44	-0.45	0.00	0.42	0.60	xh	photoreceptor cell development
GO:0042462	1.08	0.47	-0.46	0.00	0.40	0.59	xh	eye photoreceptor cell development
GO:0007586	0.44	0.02	0.11	0.00	0.92	0.53	xh	digestion
GO:0002274	0.88	0.52	-0.32	0.00	0.17	0.63	xh	myeloid leukocyte activation
GO:0001525	0.33	0.03	-0.00	0.00	0.85	0.99	xh	angiogenesis
GO:0050792	0.93	-0.14	0.01	0.02	0.84	0.99	xh	regulation of viral reproduction
GO:0045069	1.46	0.55	-0.40	0.00	0.51	0.75	xh	regulation of viral genome replication
GO:0007159	0.97	0.26	-0.17	0.04	0.73	0.90	xh	leukocyte adhesion
GO:0007416	0.65	-0.20	-0.07	0.03	0.64	0.94	xh	synaptogenesis
GO:0045576	1.39	0.05	-0.11	0.00	0.96	0.94	xh	mast cell activation
GO:0006007	0.54	0.12	-0.02	0.00	0.66	0.99	xh	glucose catabolic process
GO:0016052	0.43	0.06	0.05	0.00	0.78	0.82	xh	carbohydrate catabolic process
GO:0019320	0.53	0.13	0.01	0.00	0.55	0.99	xh	hexose catabolic process
GO:0044275	0.43	0.06	0.05	0.00	0.78	0.82	xh	cellular carbohydrate catabolic process
GO:0046164	0.48	0.02	0.09	0.00	0.94	0.69	xh	alcohol catabolic process
GO:0046365	0.53	0.13	0.01	0.00	0.55	0.99	xh	monosaccharide catabolic process
GO:0006096	0.64	-0.02	0.05	0.00	0.95	0.90	xh	glycolysis
GO:0044259	0.83	-0.34	0.06	0.02	0.42	0.94	xh	multicellular organismal macromolecule metabolic process
GO:0044236	0.86	-0.48	0.11	0.00	0.12	0.81	xh	multicellular organismal metabolic process
GO:0044243	0.91	-0.39	0.04	0.01	0.32	0.97	xh	multicellular organismal catabolic process
GO:0044256	0.83	-0.34	0.06	0.02	0.42	0.94	xh	protein digestion
GO:0044266	0.83	-0.34	0.06	0.02	0.42	0.94	xh	multicellular organismal macromolecule catabolic process
GO:0044268	0.83	-0.34	0.06	0.02	0.42	0.94	xh	multicellular organismal protein metabolic process
GO:0044254	0.83	-0.34	0.06	0.02	0.42	0.94	xh	multicellular organismal protein catabolic process
GO:0030574	0.83	-0.34	0.06	0.02	0.42	0.94	xh	collagen catabolic process
GO:0009617	0.54	0.10	0.10	0.00	0.70	0.69	xh	response to bacterium
GO:0042742	0.53	0.05	0.14	0.01	0.85	0.49	xh	defense response to bacterium
GO:0043010	1.43	-0.40	0.11	0.00	0.62	0.93	xh	camera-type eye development
GO:0051606	0.64	-0.10	-0.18	0.00	0.78	0.73	xh	detection of stimulus
GO:0009581	0.92	-0.16	-0.22	0.00	0.73	0.78	xh	detection of external stimulus
GO:0000270	0.90	-0.02	-0.05	0.00	0.97	0.97	xh	peptidoglycan metabolic process
GO:0043542	1.13	-0.10	0.29	0.01	0.86	0.48	xh	endothelial cell migration
GO:0051208	1.53	0.85	-0.52	0.00	0.22	0.60	xh	sequestering of calcium ion
GO:0051238	1.24	-0.59	0.18	0.00	0.18	0.72	xh	sequestering of metal ion
GO:0009306	0.52	-0.18	-0.02	0.02	0.53	0.99	xh	protein secretion
GO:0009582	0.77	-0.24	-0.31	0.00	0.56	0.66	xh	detection of abiotic stimulus
GO:0050906	0.81	-0.20	-0.40	0.00	0.69	0.58	xh	detection of stimulus involved in sensory perception
GO:0009583	0.92	-0.14	-0.26	0.00	0.83	0.80	xh	detection of light stimulus
GO:0009584	0.92	-0.14	-0.26	0.00	0.83	0.80	xh	detection of visible light
GO:0050962	0.93	-0.16	-0.25	0.00	0.81	0.80	xh	detection of light stimulus involved in sensory perception
GO:0007602	0.97	-0.19	-0.23	0.00	0.78	0.82	xh	phototransduction
GO:0050908	0.93	-0.16	-0.25	0.00	0.81	0.80	xh	detection of light stimulus involved in visual perception
GO:0002504	1.21	-0.18	-0.11	0.00	0.79	0.93	xh	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0045045	-0.24	0.13	-0.01	0.00	0.16	0.99	xl	establishment and/or maintenance of chromatin architecture
GO:0006325	-0.16	-0.05	-0.04	0.04	0.63	0.81	xl	
GO:0051276	-0.15	0.06	-0.00	0.03	0.48	0.99	xl	chromosome organization and biogenesis
GO:0016568	-0.35	-0.01	-0.09	0.00	0.98	0.65	xl	chromatin modification
GO:0007264	-0.14	0.08	0.07	0.05	0.34	0.40	xl	small GTPase mediated signal transduction
GO:0006631	-0.25	-0.12	-0.06	0.01	0.39	0.80	xl	fatty acid metabolic process
GO:0008202	-0.22	0.11	-0.01	0.03	0.37	0.97	xl	steroid metabolic process
GO:0030183	-0.41	0.37	0.01	0.04	0.06	0.99	xl	B cell differentiation
GO:0045786	-0.26	-0.04	0.05	0.00	0.73	0.78	xl	negative regulation of cell cycle
GO:0007179	-0.38	-0.37	-0.32	0.05	0.12	0.39	xl	transforming growth factor beta receptor signaling pathway
GO:0008610	-0.24	-0.06	-0.09	0.00	0.66	0.58	xl	lipid biosynthetic process
GO:0007050	-0.35	-0.16	0.02	0.01	0.39	0.98	xl	cell cycle arrest
GO:0048193	-0.41	0.20	0.01	0.00	0.10	0.99	xl	Golgi vesicle transport
GO:0006473	-0.76	-0.49	-0.44	0.00	0.15	0.26	xl	protein amino acid acetylation
GO:0016569	-0.54	-0.19	-0.37	0.00	0.55	0.23	xl	covalent chromatin modification
GO:0016570	-0.54	-0.19	-0.37	0.00	0.55	0.23	xl	histone modification
GO:0043543	-0.67	-0.44	-0.32	0.00	0.14	0.47	xl	protein amino acid acylation
GO:0032273	-0.81	0.66	-0.04	0.03	0.07	0.97	xl	positive regulation of protein polymerization
GO:0051495	-0.69	0.50	-0.00	0.02	0.13	0.99	xl	positive regulation of cytoskeleton organization and biogenesis
GO:0030518	-0.35	0.05	-0.02	0.03	0.84	0.98	xl	steroid hormone receptor signaling pathway
GO:0030522	-0.34	0.03	-0.02	0.03	0.89	0.99	xl	intracellular receptor-mediated signaling pathway
GO:0006694	-0.39	0.16	-0.11	0.00	0.42	0.77	xl	steroid biosynthetic process

GO:0045682	-0.78	0.07	0.03	0.02	0.91	0.99	xl	regulation of epidermis development
GO:0006505	-0.65	-0.39	-0.26	0.02	0.39	0.73	xl	GPI anchor metabolic process
GO:0006506	-0.65	-0.39	-0.26	0.02	0.39	0.73	xl	GPI anchor biosynthetic process
GO:0030384	-0.44	-0.13	-0.14	0.03	0.73	0.80	xl	phosphoinositide metabolic process
GO:0000245	-0.42	0.26	-0.22	0.03	0.31	0.63	xl	spliceosome assembly
GO:0006376	-0.66	0.34	-0.20	0.01	0.38	0.78	xl	mRNA splice site selection
GO:0006383	-0.45	0.18	-0.09	0.05	0.59	0.88	xl	transcription from RNA polymerase III promoter
GO:0009081	-0.82	0.47	-0.10	0.00	0.26	0.91	xl	branched chain family amino acid metabolic process
GO:0016126	-0.69	0.42	-0.17	0.00	0.08	0.72	xl	sterol biosynthetic process
GO:0006695	-0.70	0.08	-0.37	0.00	0.85	0.47	xl	cholesterol biosynthetic process
GO:0048515	-0.51	-0.02	-0.17	0.03	0.97	0.80	xl	spermatid differentiation
GO:0015669	-0.89	-0.63	-0.50	0.00	0.19	0.45	xl	gas transport
GO:0015671	-0.89	-0.63	-0.50	0.00	0.19	0.45	xl	oxygen transport
GO:0010212	-0.79	0.14	-0.32	0.03	0.85	0.78	xl	response to ionizing radiation
GO:0007031	-0.59	-0.13	-0.19	0.01	0.80	0.79	xl	peroxisome organization and biogenesis
GO:0001542	-0.79	0.43	-0.26	0.05	0.51	0.81	xl	ovulation from ovarian follicle
GO:0030728	-0.84	0.54	-0.30	0.03	0.35	0.78	xl	ovulation
GO:0006414	-0.69	0.37	-0.18	0.00	0.29	0.78	xl	translational elongation
GO:0006163	0.18	0.34	-0.22	0.35	0.04	0.48	yh	purine nucleotide metabolic process
GO:0006144	0.93	0.98	-0.50	0.10	0.00	0.47	yh	purine base metabolic process
GO:0009259	0.11	0.34	-0.17	0.58	0.03	0.59	yh	ribonucleotide metabolic process
GO:0045944	-0.19	0.25	-0.09	0.09	0.01	0.66	yh	positive regulation of transcription from RNA polymerase II promoter
GO:0006520	0.03	0.20	0.01	0.81	0.02	0.97	yh	amino acid metabolic process
GO:0032268	-0.10	0.21	0.10	0.29	0.00	0.06	yh	regulation of cellular protein metabolic process
GO:0032270	0.18	0.32	-0.09	0.31	0.04	0.78	yh	positive regulation of cellular protein metabolic process
GO:0051246	-0.10	0.21	0.09	0.26	0.00	0.13	yh	regulation of protein metabolic process
GO:0051247	0.16	0.30	-0.09	0.37	0.05	0.79	yh	positive regulation of protein metabolic process
GO:0009889	-0.19	0.21	0.01	0.06	0.03	0.97	yh	regulation of biosynthetic process
GO:0031326	-0.19	0.21	0.01	0.06	0.03	0.97	yh	regulation of cellular biosynthetic process
GO:0001775	0.16	0.25	-0.05	0.13	0.01	0.81	yh	cell activation
GO:0045321	0.15	0.26	-0.04	0.19	0.01	0.84	yh	leukocyte activation
GO:0046649	0.13	0.25	-0.03	0.28	0.01	0.93	yh	lymphocyte activation
GO:0050854	0.48	0.74	-0.34	0.38	0.04	0.67	yh	regulation of antigen receptor-mediated signaling pathway
GO:0050856	0.48	0.74	-0.34	0.38	0.04	0.67	yh	regulation of T cell receptor signaling pathway
GO:0051094	-0.06	0.21	0.03	0.49	0.00	0.79	yh	positive regulation of developmental process
GO:0043068	-0.07	0.27	0.04	0.52	0.00	0.80	yh	positive regulation of programmed cell death
GO:0006417	-0.21	0.29	0.02	0.05	0.00	0.93	yh	regulation of translation
GO:0042098	0.02	0.43	-0.07	0.95	0.05	0.90	yh	T cell proliferation
GO:0001816	0.13	0.32	-0.10	0.47	0.03	0.75	yh	cytokine production
GO:0042089	0.06	0.36	-0.13	0.82	0.04	0.75	yh	cytokine biosynthetic process
GO:0042107	0.07	0.35	-0.13	0.79	0.05	0.75	yh	cytokine metabolic process
GO:0043065	-0.07	0.27	0.04	0.51	0.00	0.80	yh	positive regulation of apoptosis
GO:0007243	0.09	0.16	0.01	0.28	0.03	0.95	yh	protein kinase cascade
GO:0051052	0.07	0.41	-0.16	0.76	0.01	0.60	yh	regulation of DNA metabolic process
GO:0043388	-0.21	0.77	-0.16	0.59	0.00	0.73	yh	positive regulation of DNA binding
GO:0051090	-0.28	0.49	-0.06	0.24	0.01	0.90	yh	regulation of transcription factor activity
GO:0051091	-0.23	0.84	-0.16	0.58	0.00	0.75	yh	positive regulation of transcription factor activity
GO:0051099	-0.25	0.73	-0.14	0.48	0.00	0.78	yh	positive regulation of binding
GO:0051101	-0.28	0.45	-0.08	0.18	0.01	0.82	yh	regulation of DNA binding
GO:0007249	0.15	0.36	-0.05	0.30	0.00	0.82	yh	I-kappaB kinase/NF-kappaB cascade
GO:0006282	-0.43	0.93	-0.21	0.47	0.00	0.78	yh	regulation of DNA repair
GO:0051092	0.01	0.86	-0.23	0.99	0.00	0.67	yh	positive regulation of NF-kappaB transcription factor activity
GO:0030099	-0.10	0.26	0.01	0.56	0.05	0.97	yh	myeloid cell differentiation
GO:0030218	-0.40	0.42	-0.02	0.06	0.04	0.97	yh	erythrocyte differentiation
GO:0034101	-0.40	0.42	-0.02	0.06	0.04	0.97	yh	erythrocyte homeostasis
GO:0048534	-0.07	0.18	0.03	0.59	0.05	0.84	yh	hemopoietic or lymphoid organ development
GO:0048872	-0.28	0.46	-0.06	0.17	0.01	0.88	yh	homeostasis of number of cells
GO:0043069	-0.04	0.19	0.05	0.76	0.02	0.72	yh	negative regulation of programmed cell death
GO:0007260	0.34	0.78	-0.15	0.48	0.01	0.80	yh	tyrosine phosphorylation of STAT protein
GO:0043066	-0.04	0.20	0.05	0.73	0.01	0.73	yh	negative regulation of apoptosis
GO:0017038	-0.25	0.41	-0.02	0.05	0.00	0.95	yh	protein import
GO:0051170	-0.25	0.39	-0.03	0.06	0.00	0.94	yh	nuclear import
GO:0009057	-0.03	0.15	0.04	0.74	0.03	0.75	yh	macromolecule catabolic process
GO:0022404	-0.38	0.65	-0.28	0.31	0.02	0.63	yh	molting cycle process
GO:0042303	-0.32	0.65	-0.27	0.42	0.01	0.63	yh	molting cycle
GO:0042633	-0.32	0.65	-0.27	0.42	0.01	0.63	yh	hair cycle
GO:0007005	0.10	0.32	0.02	0.65	0.03	0.97	yh	mitochondrion organization and biogenesis
GO:0008632	0.17	0.31	0.04	0.37	0.05	0.89	yh	apoptotic program
GO:0022405	-0.38	0.65	-0.28	0.31	0.02	0.63	yh	hair cycle process
GO:0001942	-0.38	0.65	-0.28	0.31	0.02	0.63	yh	hair follicle development
GO:0006916	-0.07	0.22	0.06	0.52	0.01	0.67	yh	anti-apoptosis
GO:0065002	-0.23	0.53	-0.01	0.44	0.01	0.99	yh	intracellular protein transport across a membrane
GO:0000060	-0.23	0.53	-0.01	0.44	0.01	0.99	yh	protein import into nucleus, translocation
GO:0009615	0.17	0.34	0.07	0.35	0.02	0.78	yh	response to virus
GO:0006405	-0.20	0.44	-0.12	0.47	0.04	0.80	yh	RNA export from nucleus
GO:0051168	-0.18	0.51	-0.13	0.40	0.00	0.72	yh	nuclear export
GO:0012502	-0.05	0.26	0.04	0.70	0.00	0.81	yh	induction of programmed cell death
GO:0051325	-0.23	0.38	0.10	0.13	0.00	0.50	yh	interphase
GO:0051329	-0.23	0.39	0.10	0.12	0.00	0.48	yh	interphase of mitotic cell cycle
GO:0006917	-0.05	0.26	0.04	0.68	0.00	0.81	yh	induction of apoptosis
GO:0042254	0.09	0.34	0.00	0.71	0.04	0.99	yh	ribosome biogenesis
GO:0006611	-0.17	0.60	-0.15	0.69	0.02	0.80	yh	protein export from nucleus
GO:0006260	-0.13	0.28	0.06	0.22	0.00	0.63	yh	DNA replication
GO:0031570	-0.21	0.59	0.01	0.37	0.00	0.99	yh	DNA integrity checkpoint
GO:0042770	-0.10	0.54	0.03	0.66	0.00	0.93	yh	DNA damage response, signal transduction
GO:0000077	-0.26	0.57	0.02	0.25	0.00	0.97	yh	DNA damage checkpoint
GO:0009314	-0.11	0.30	0.10	0.52	0.03	0.50	yh	response to radiation
GO:0007126	-0.12	0.34	0.01	0.56	0.03	0.99	yh	meiosis
GO:0051321	-0.11	0.35	0.01	0.59	0.02	0.99	yh	meiotic cell cycle
GO:0051327	-0.12	0.34	0.01	0.56	0.03	0.99	yh	M phase of meiotic cell cycle
GO:0051262	-0.43	0.55	-0.06	0.13	0.02	0.93	yh	protein tetramerization
GO:0006261	-0.04	0.29	-0.02	0.86	0.03	0.95	yh	DNA-dependent DNA replication
GO:0046466	-0.39	0.53	0.14	0.21	0.02	0.60	yh	membrane lipid catabolic process
GO:0007164	-0.61	0.84	-0.30	0.26	0.02	0.71	yh	establishment of tissue polarity
GO:0000226	-0.12	0.29	0.12	0.48	0.03	0.38	yh	microtubule cytoskeleton organization and biogenesis
GO:0007017	-0.02	0.23	0.11	0.90	0.01	0.15	yh	microtubule-based process
GO:0032271	-0.46	0.58	-0.03	0.15	0.03	0.98	yh	regulation of protein polymerization
GO:0007346	-0.21	0.36	0.10	0.22	0.01	0.49	yh	regulation of mitotic cell cycle
GO:0007067	-0.11	0.41	0.12	0.32	0.00	0.09	yh	mitosis
GO:0007088	-0.08	0.47	0.07	0.76	0.00	0.78	yh	regulation of mitosis

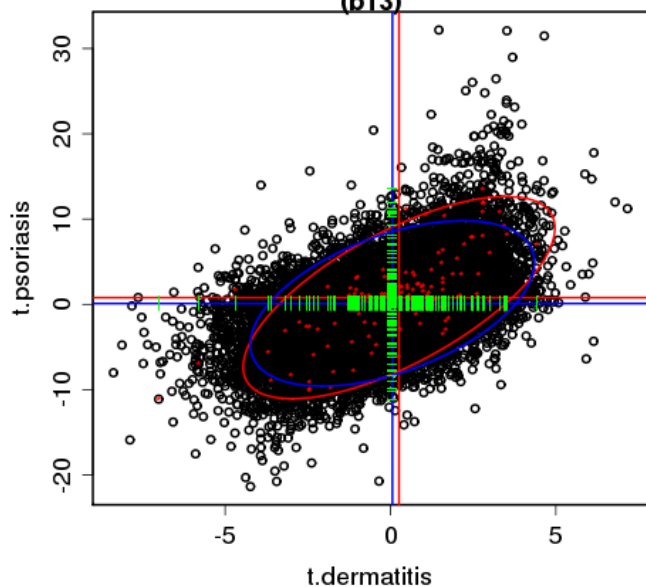
GO:0006767	-0.08	0.45	-0.10	0.81	0.03	0.82	yh	water-soluble vitamin metabolic process
GO:0006769	0.11	0.59	-0.14	0.81	0.05	0.82	yh	nicotinamide metabolic process
GO:0006691	-0.30	0.62	-0.19	0.48	0.04	0.80	yh	leukotriene metabolic process
GO:0043449	-0.30	0.62	-0.19	0.48	0.04	0.80	yh	alkene metabolic process
GO:0043450	-0.39	0.65	-0.17	0.36	0.04	0.81	yh	alkene biosynthetic process
GO:0019370	-0.39	0.65	-0.17	0.36	0.04	0.81	yh	leukotriene biosynthetic process
GO:0046034	0.04	0.43	-0.29	0.88	0.04	0.48	yh	ATP metabolic process
GO:0044265	-0.08	0.18	0.07	0.40	0.02	0.48	yh	cellular macromolecule catabolic process
GO:0045840	0.96	1.18	-0.44	0.23	0.00	0.56	yh	positive regulation of mitosis
GO:0001906	0.23	0.67	-0.15	0.64	0.03	0.82	yh	cell killing
GO:0001909	0.33	0.68	-0.15	0.51	0.05	0.82	yh	leukocyte mediated cytotoxicity
GO:0002228	0.33	0.68	-0.15	0.51	0.05	0.82	yh	natural killer cell mediated immunity
GO:0042267	0.33	0.68	-0.15	0.51	0.05	0.82	yh	natural killer cell mediated cytotoxicity
GO:0006984	-0.50	0.55	0.07	0.14	0.05	0.90	yh	ER-nuclear signaling pathway
GO:0045639	-0.27	0.53	-0.27	0.41	0.03	0.60	yh	positive regulation of myeloid cell differentiation
GO:0030833	-0.47	0.71	-0.10	0.23	0.01	0.89	yh	regulation of actin filament polymerization
GO:0006818	-0.00	0.43	-0.17	1.00	0.01	0.61	yh	hydrogen transport
GO:0015992	0.02	0.36	-0.16	0.94	0.04	0.67	yh	proton transport
GO:0006275	0.04	0.50	-0.19	0.92	0.05	0.75	yh	regulation of DNA replication
GO:0045648	-0.61	1.06	-0.29	0.25	0.00	0.60	yh	positive regulation of erythrocyte differentiation
GO:0006270	-0.04	0.56	-0.04	0.91	0.01	0.94	yh	DNA replication initiation
GO:0002456	-0.08	0.79	-0.13	0.91	0.01	0.85	yh	T cell mediated immunity
GO:0051648	-0.05	0.52	0.01	0.91	0.05	0.99	yh	vesicle localization
GO:0051650	-0.07	0.53	0.02	0.87	0.05	0.99	yh	establishment of vesicle localization
GO:0048730	-0.38	0.46	0.13	0.08	0.01	0.51	yh	epidermis morphogenesis
GO:0009411	-0.36	0.62	0.13	0.19	0.00	0.61	yh	response to UV
GO:0048284	-0.20	0.72	-0.11	0.77	0.05	0.91	yh	organelle fusion
GO:0008634	-0.55	0.82	-0.11	0.24	0.01	0.88	yh	negative regulation of survival gene product expression
GO:0008053	-0.34	0.76	-0.07	0.59	0.04	0.94	yh	mitochondrial fusion
GO:0006739	-0.02	0.67	-0.20	0.99	0.03	0.79	yh	NADP metabolic process
GO:0001819	0.33	0.65	-0.35	0.47	0.04	0.60	yh	positive regulation of cytokine production
GO:0000086	-0.09	0.61	0.01	0.85	0.03	0.99	yh	G2/M transition of mitotic cell cycle
GO:0007059	-0.16	0.47	0.04	0.52	0.01	0.93	yh	chromosome segregation
GO:0031069	-0.27	0.89	-0.26	0.73	0.00	0.77	yh	hair follicle morphogenesis
GO:0006302	-0.24	0.52	-0.11	0.37	0.01	0.81	yh	double-strand break repair
GO:0007032	-0.40	1.16	-0.33	0.56	0.00	0.54	yh	endosome organization and biogenesis
GO:0007051	0.33	0.55	0.04	0.37	0.05	0.95	yh	spindle organization and biogenesis
GO:0032635	0.37	0.97	-0.56	0.65	0.00	0.39	yh	interleukin-6 production
GO:0042226	0.37	0.97	-0.56	0.65	0.00	0.39	yh	interleukin-6 biosynthetic process
GO:0008593	-0.69	0.82	-0.15	0.06	0.00	0.80	yh	regulation of Notch signaling pathway
GO:0030330	0.27	0.62	-0.07	0.52	0.03	0.93	yh	DNA damage response, signal transduction by p53 class mediator
GO:0030968	-0.61	0.72	0.01	0.10	0.01	0.99	yh	endoplasmic reticulum unfolded protein response
GO:0046479	0.43	0.91	-0.15	0.60	0.03	0.87	yh	glycosphingolipid catabolic process
GO:0006829	0.02	0.78	-0.36	0.98	0.04	0.71	yh	zinc ion transport
GO:0007020	-0.76	0.75	-0.22	0.06	0.04	0.78	yh	microtubule nucleation
GO:0001501	0.12	-0.19	0.01	0.25	0.04	0.99	yl	skeletal development
GO:0003012	0.05	-0.28	-0.10	0.72	0.01	0.67	yl	muscle system process
GO:0006936	0.05	-0.28	-0.10	0.72	0.01	0.67	yl	muscle contraction
GO:0019226	0.13	-0.25	-0.14	0.14	0.00	0.24	yl	transmission of nerve impulse
GO:0006939	0.11	-0.49	-0.10	0.74	0.04	0.85	yl	smooth muscle contraction
GO:0007417	-0.09	-0.22	0.03	0.44	0.02	0.90	yl	central nervous system development
GO:0022008	0.11	-0.30	0.02	0.27	0.00	0.90	yl	neurogenesis
GO:0048699	0.15	-0.32	0.02	0.12	0.00	0.93	yl	generation of neurons
GO:0007420	0.01	-0.25	-0.02	0.97	0.05	0.96	yl	brain development
GO:0030900	-0.02	-0.56	-0.10	0.95	0.01	0.82	yl	forebrain development
GO:0008285	-0.05	-0.19	0.03	0.70	0.04	0.87	yl	negative regulation of cell proliferation
GO:0021700	0.09	-0.32	-0.04	0.66	0.05	0.93	yl	developmental maturation
GO:0032990	0.13	-0.20	-0.01	0.24	0.05	0.99	yl	cell part morphogenesis
GO:0030030	0.13	-0.20	-0.01	0.24	0.05	0.99	yl	cell projection organization and biogenesis
GO:0031175	0.15	-0.24	0.03	0.28	0.03	0.93	yl	neurite development
GO:0048666	0.18	-0.26	0.01	0.13	0.01	0.99	yl	neuron development
GO:0048858	0.13	-0.20	-0.01	0.24	0.05	0.99	yl	cell projection morphogenesis
GO:0007517	0.03	-0.33	0.00	0.84	0.00	0.99	yl	muscle development
GO:0014706	0.01	-0.30	-0.02	0.95	0.03	0.97	yl	striated muscle development
GO:0008361	-0.04	-0.25	0.02	0.78	0.02	0.95	yl	regulation of cell size
GO:0040007	-0.10	-0.24	-0.05	0.34	0.01	0.81	yl	growth
GO:0016049	-0.02	-0.28	0.02	0.88	0.01	0.94	yl	cell growth
GO:0007519	0.03	-0.29	-0.03	0.90	0.05	0.94	yl	skeletal muscle development
GO:0000271	0.20	-0.59	-0.11	0.63	0.04	0.90	yl	polysaccharide biosynthetic process
GO:0033692	0.20	-0.59	-0.11	0.63	0.04	0.90	yl	cellular polysaccharide biosynthetic process
GO:0007268	0.14	-0.26	-0.18	0.12	0.00	0.13	yl	synaptic transmission
GO:0009566	0.06	-0.48	-0.30	0.82	0.03	0.51	yl	fertilization
GO:0007338	0.06	-0.48	-0.29	0.82	0.03	0.53	yl	single fertilization
GO:0048741	0.23	-0.44	-0.04	0.30	0.01	0.95	yl	skeletal muscle fiber development
GO:0048747	0.23	-0.44	-0.04	0.30	0.01	0.95	yl	muscle fiber development
GO:0030239	0.74	-0.95	0.08	0.06	0.00	0.90	yl	myofibril assembly
GO:0045445	0.38	-0.50	0.01	0.15	0.02	0.99	yl	myoblast differentiation
GO:0051146	0.37	-0.69	0.01	0.35	0.02	0.99	yl	striated muscle cell differentiation
GO:0055001	0.74	-0.95	0.08	0.06	0.00	0.90	yl	muscle cell development
GO:0055002	0.74	-0.95	0.08	0.06	0.00	0.90	yl	striated muscle cell development
GO:0040008	0.02	-0.30	-0.01	0.88	0.00	0.97	yl	regulation of growth
GO:0035295	0.19	-0.24	0.06	0.18	0.04	0.78	yl	tube development
GO:0006022	0.18	-0.61	-0.15	0.52	0.00	0.77	yl	aminoglycan metabolic process
GO:0030203	0.16	-0.58	-0.14	0.56	0.00	0.78	yl	glycosaminoglycan metabolic process
GO:0001558	0.07	-0.29	0.01	0.70	0.01	0.98	yl	regulation of cell growth
GO:0003013	0.17	-0.39	-0.06	0.18	0.00	0.81	yl	circulatory system process
GO:0008015	0.17	-0.39	-0.06	0.18	0.00	0.81	yl	blood circulation
GO:0002541	0.50	-0.58	-0.07	0.08	0.01	0.93	yl	activation of plasma proteins during acute inflammatory response
GO:0006956	0.50	-0.58	-0.07	0.08	0.01	0.93	yl	complement activation
GO:0006575	0.27	-0.30	0.10	0.13	0.04	0.63	yl	amino acid derivative metabolic process
GO:0018958	0.19	-0.63	-0.25	0.58	0.01	0.68	yl	phenol metabolic process
GO:0003018	0.29	-0.49	-0.06	0.34	0.05	0.94	yl	vascular process in circulatory system
GO:0019229	0.59	-1.12	-0.14	0.36	0.00	0.90	yl	regulation of vasoconstriction
GO:0035150	0.32	-0.50	-0.05	0.30	0.04	0.95	yl	regulation of tube size
GO:0042310	0.51	-0.80	-0.10	0.27	0.01	0.93	yl	vasoconstriction
GO:0050880	0.32	-0.50	-0.05	0.30	0.04	0.95	yl	regulation of blood vessel size
GO:0006584	0.21	-0.65	-0.24	0.54	0.01	0.71	yl	catecholamine metabolic process
GO:0019216	0.48	-0.63	0.08	0.16	0.02	0.89	yl	regulation of lipid metabolic process
GO:0030111	-0.12	-0.56	0.06	0.73	0.02	0.90	yl	regulation of Wnt receptor signaling pathway
GO:0016358	0.53	-0.52	-0.05	0.07	0.05	0.96	yl	dendrite development
GO:0006721	-0.56	-0.93	-0.34	0.25	0.02	0.67	yl	terpenoid metabolic process
GO:0016101	-0.38	-0.98	-0.28	0.52	0.02	0.78	yl	diterpenoid metabolic process
GO:0001523	-0.38	-0.98	-0.28	0.52	0.02	0.78	yl	retinoid metabolic process
GO:0006778	-0.02	-0.92	-0.46	0.99	0.00	0.46	yl	porphyrin metabolic process
GO:0033013	-0.02	-0.92	-0.46	0.99	0.00	0.46	yl	tetrapyrrole metabolic process
GO:0006779	-0.06	-0.71	-0.27	0.93	0.03	0.75	yl	porphyrin biosynthetic process

GO:0033014	-0.06	-0.71	-0.27	0.93	0.03	0.75	yl	tetrapyrrole biosynthetic process
GO:0042168	0.08	-0.93	-0.43	0.87	0.00	0.51	yl	heme metabolic process
GO:0006783	0.04	-0.71	-0.23	0.93	0.04	0.80	yl	heme biosynthetic process
GO:0006937	-0.06	-0.66	-0.11	0.89	0.01	0.84	yl	regulation of muscle contraction
GO:0001936	-0.08	-0.95	-0.23	0.92	0.02	0.81	yl	regulation of endothelial cell proliferation
GO:0006662	0.32	-0.77	-0.12	0.50	0.01	0.90	yl	glycerol ether metabolic process
GO:0009612	0.49	-0.87	-0.41	0.45	0.05	0.75	yl	response to mechanical stimulus
GO:0042311	0.74	-0.80	0.10	0.08	0.01	0.88	yl	vasodilation
GO:0006638	0.38	-0.87	-0.21	0.47	0.01	0.82	yl	neutral lipid metabolic process
GO:0006639	0.38	-0.87	-0.21	0.47	0.01	0.82	yl	acylglycerol metabolic process
GO:0046486	0.37	-0.90	-0.12	0.46	0.00	0.90	yl	glycerolipid metabolic process
GO:0030178	0.34	-0.90	0.08	0.44	0.00	0.90	yl	negative regulation of Wnt receptor signaling pathway
GO:0046928	0.11	-0.89	-0.17	0.87	0.02	0.86	yl	regulation of neurotransmitter secretion
GO:0048168	-0.46	-0.97	-0.20	0.43	0.02	0.82	yl	regulation of neuronal synaptic plasticity
GO:0007398	-0.27	0.38	0.13	0.01	0.00	0.04	no_rel	ectoderm development
GO:0000278	-0.17	0.36	0.12	0.03	0.00	0.00	no_rel	mitotic cell cycle

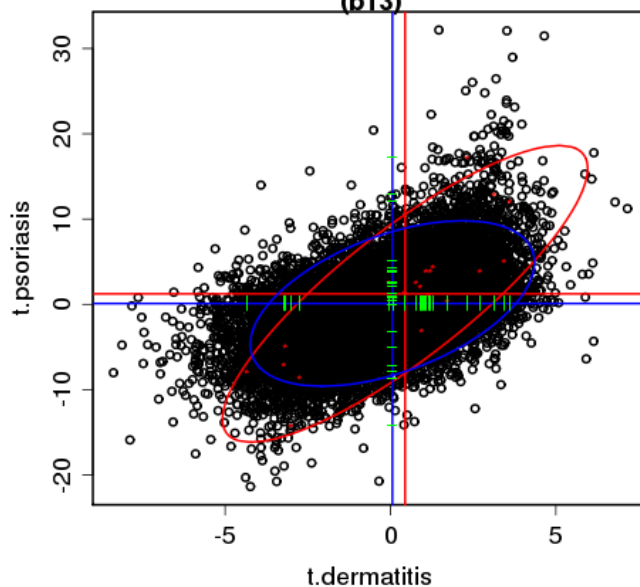
Table 1: LOR: log odds ratio; p: adjusted p-value FDR



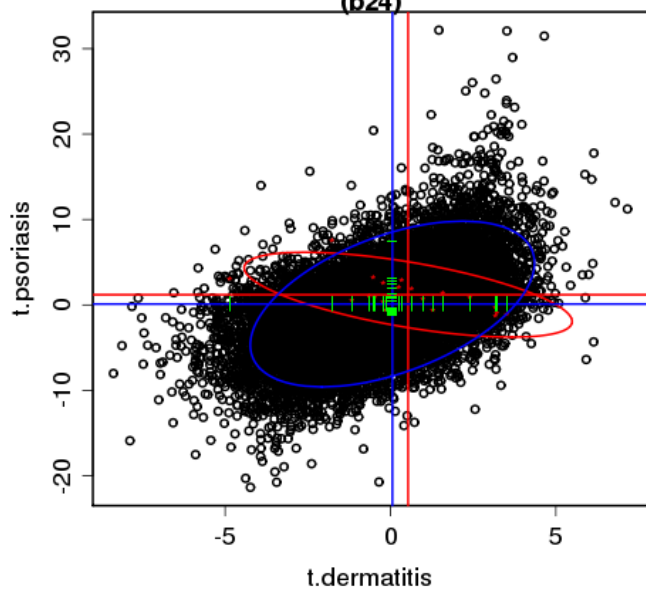
GO:0048015
phosphoinositide-mediated signaling
(b13)



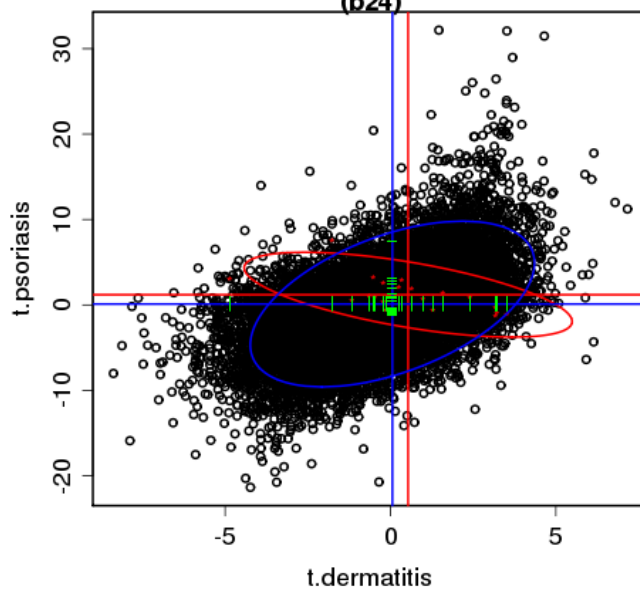
GO:0000302
response to reactive oxygen species
(b13)



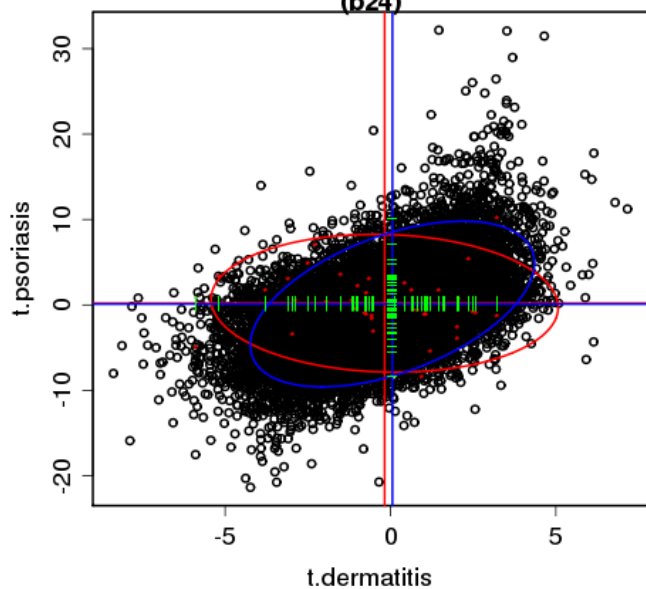
GO:0032945
negative regulation of mononuclear cell proliferation
(b24)



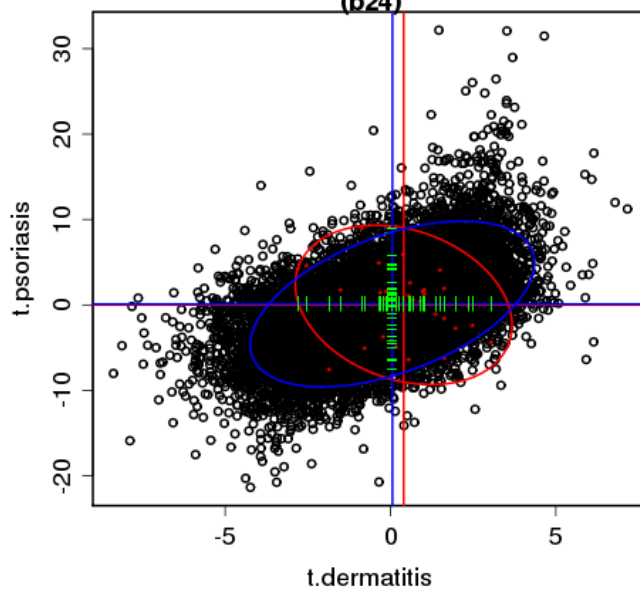
GO:0050672
negative regulation of lymphocyte proliferation
(b24)



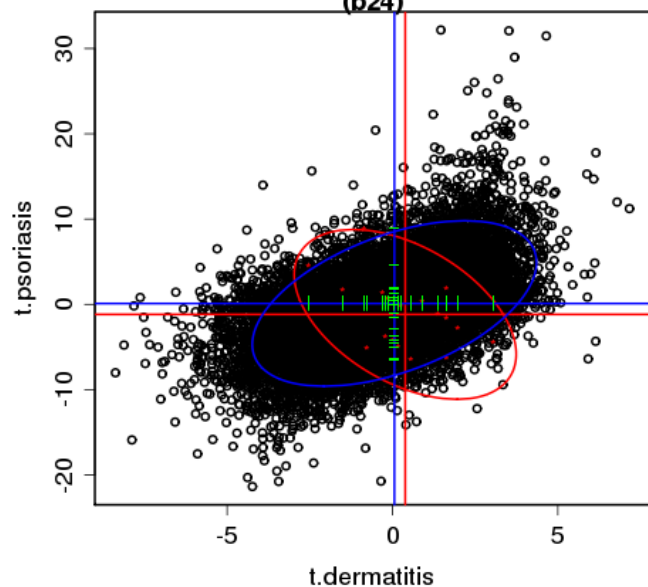
GO:0048589
developmental growth
(b24)



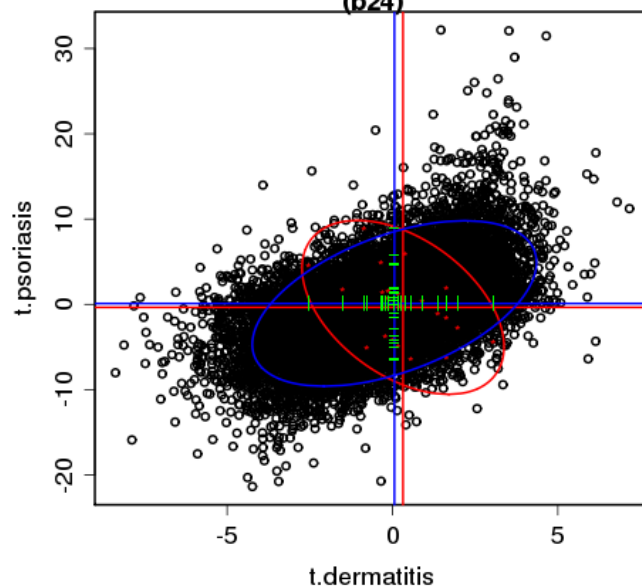
GO:0007028
cytoplasm organization and biogenesis
(b24)



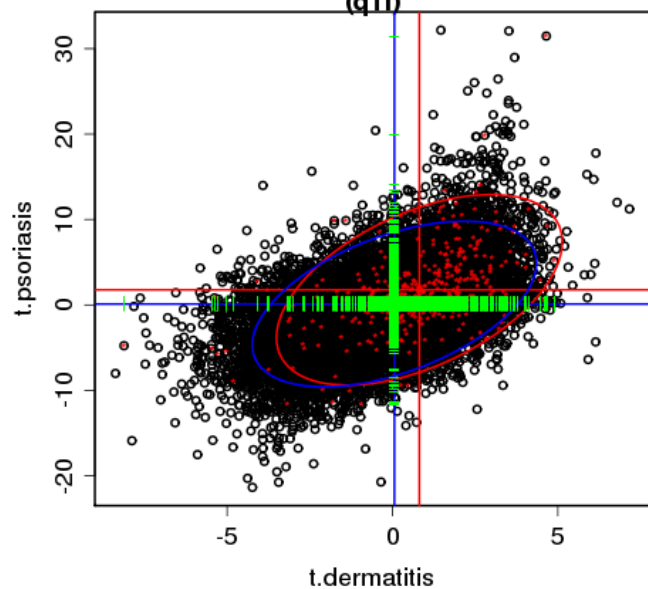
GO:0007043
cell-cell junction assembly
(b24)



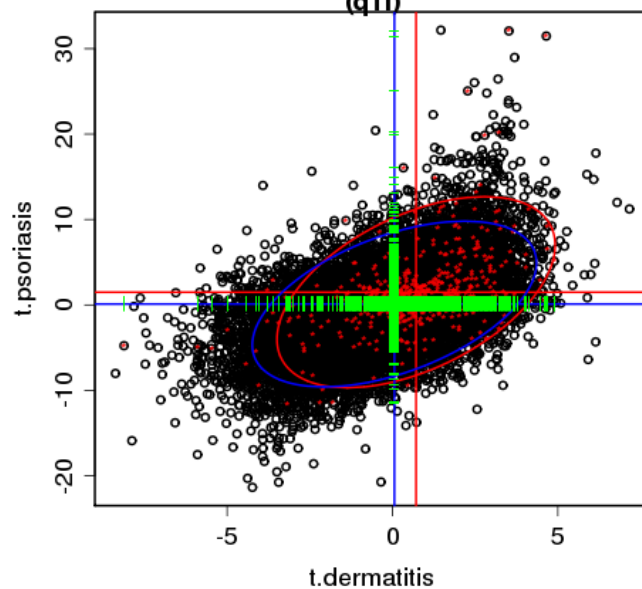
GO:0045216
cell-cell junction assembly and maintenance
(b24)



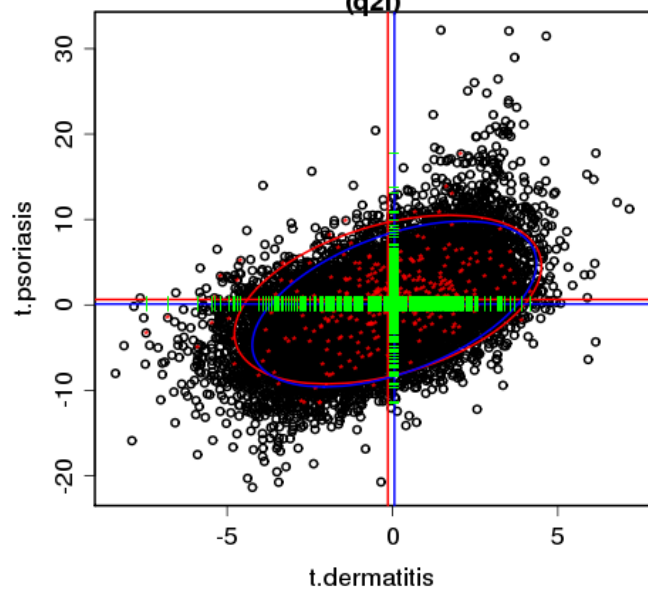
GO:0009607
response to biotic stimulus
(q1f)



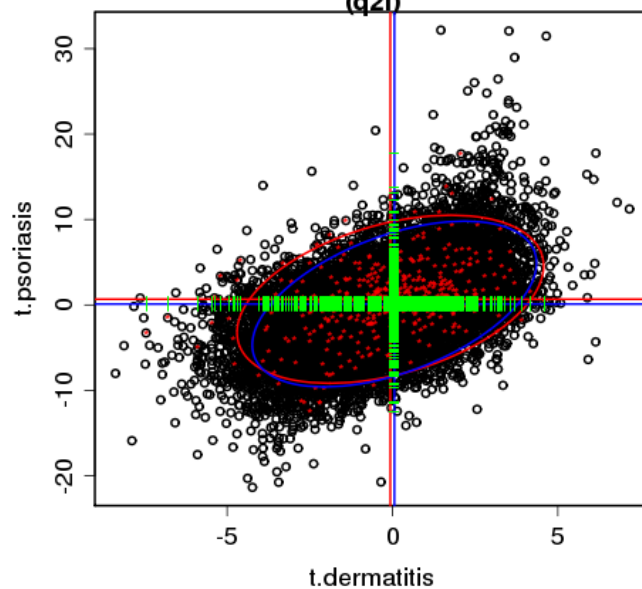
GO:0051704
multi-organism process
(q1f)



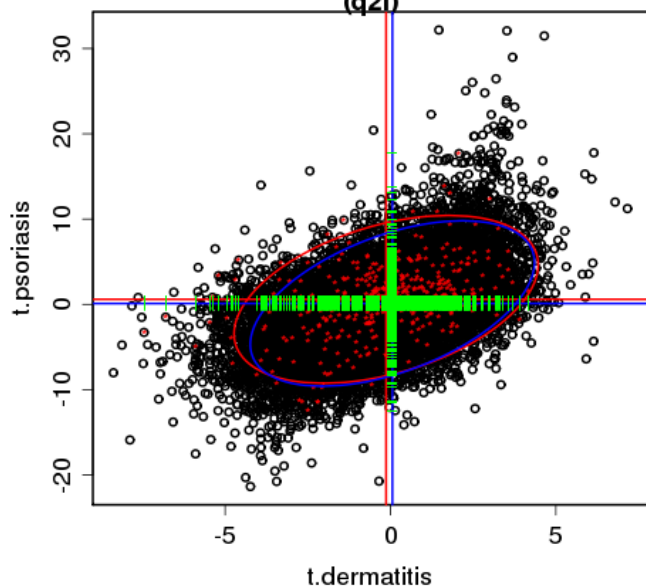
GO:0045893
positive regulation of transcription, DNA-dependent
(q2f)



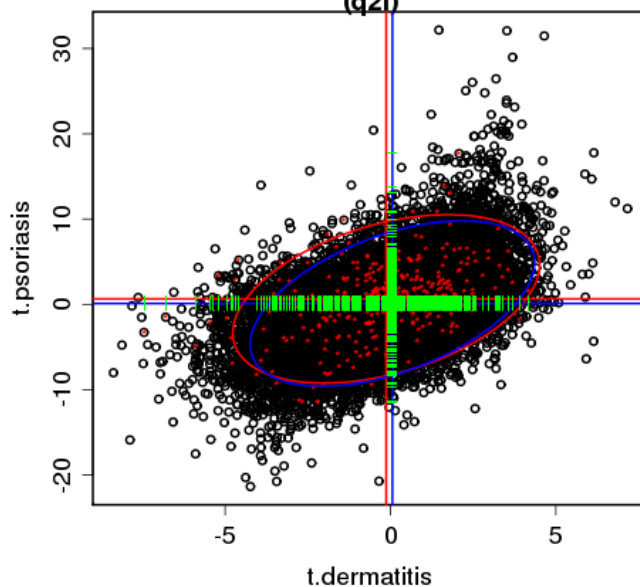
GO:0045935
nucleobase, nucleoside, nucleotide and nucleic acid metabolism
(q2f)



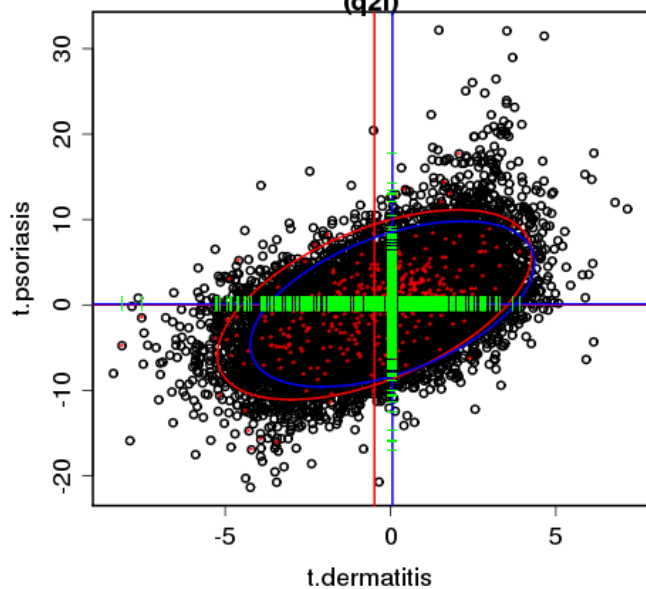
GO:0045941
positive regulation of transcription
(q2f)



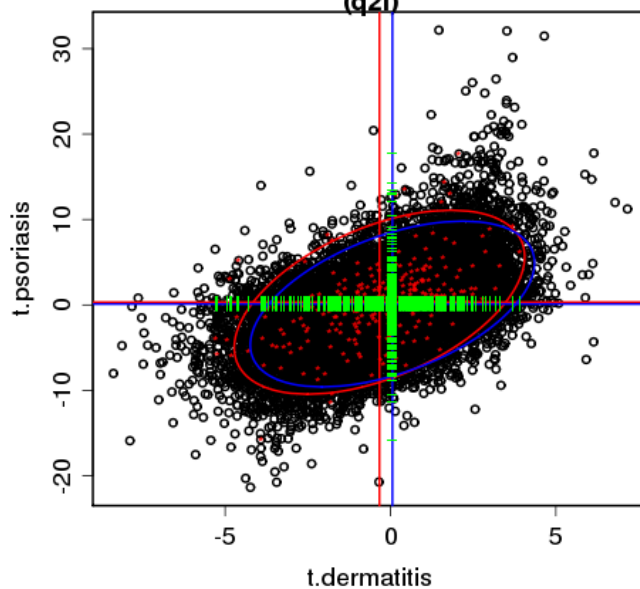
GO:0051254
positive regulation of RNA metabolic process
(q2f)



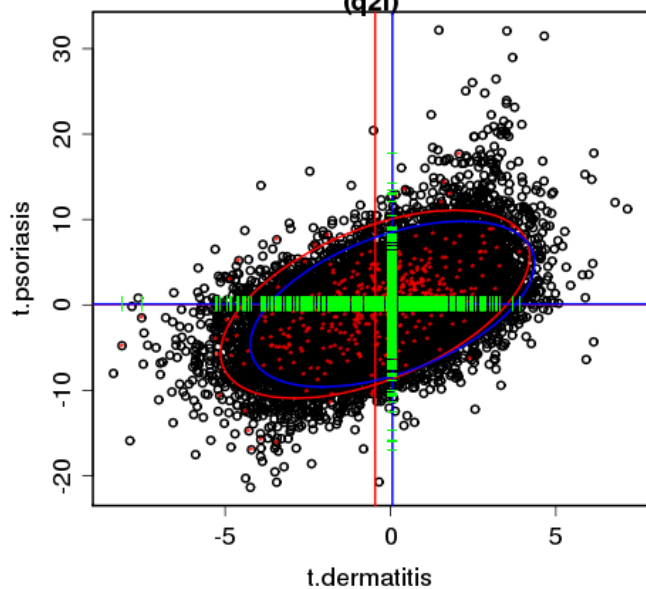
GO:0016481
negative regulation of transcription
(q2f)



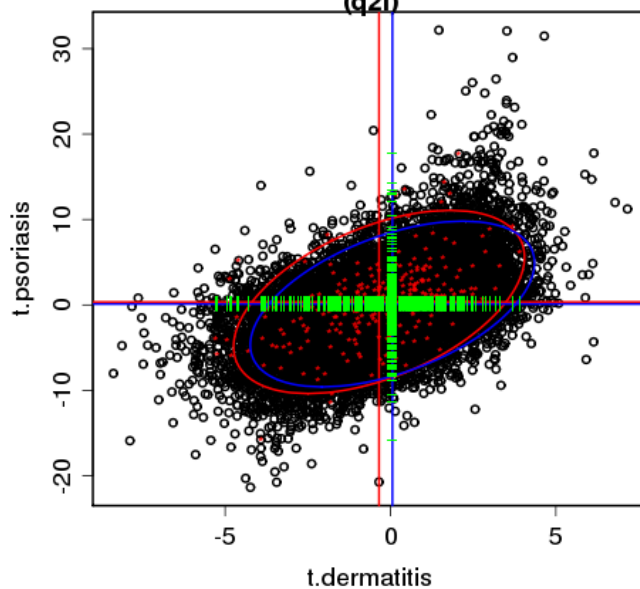
GO:0045892
negative regulation of transcription, DNA-dependent
(q2f)



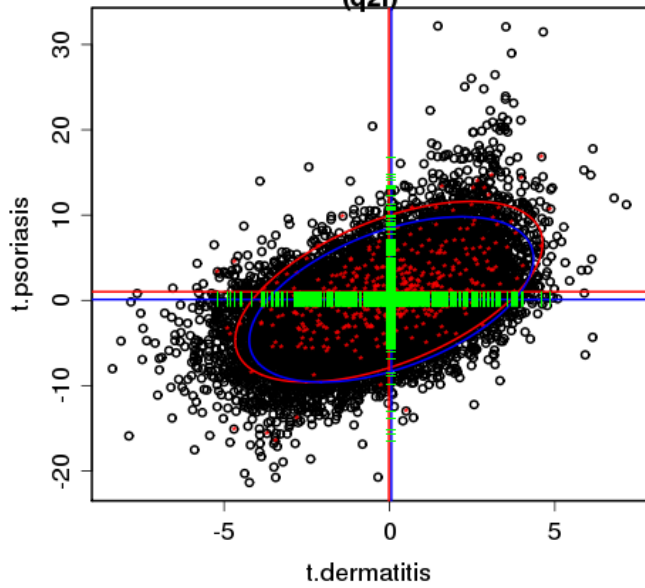
GO:0045934
synthesis of nucleobase, nucleoside, nucleotide and nucleic acid
(q2f)



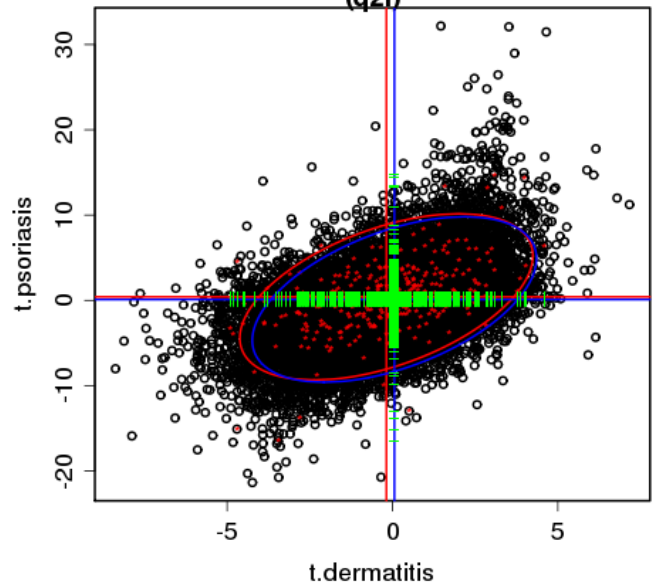
GO:0051253
negative regulation of RNA metabolic process
(q2f)



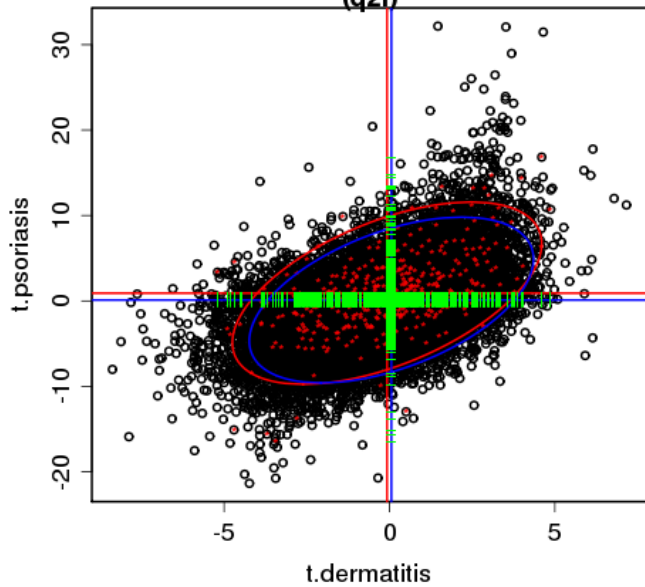
GO:0009719
response to endogenous stimulus
(q2f)



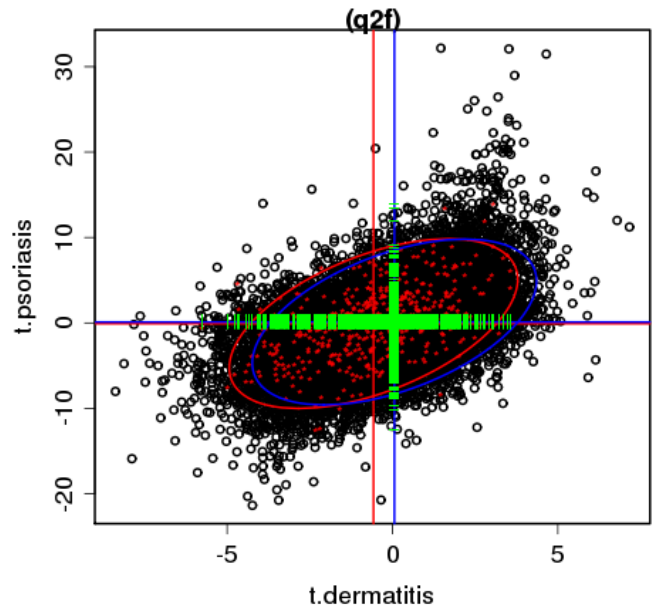
GO:0006281
DNA repair
(q2f)



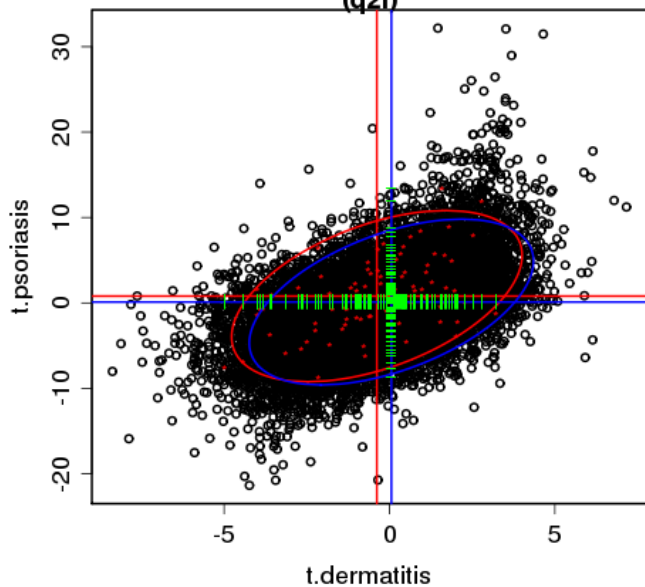
GO:0006974
response to DNA damage stimulus
(q2f)



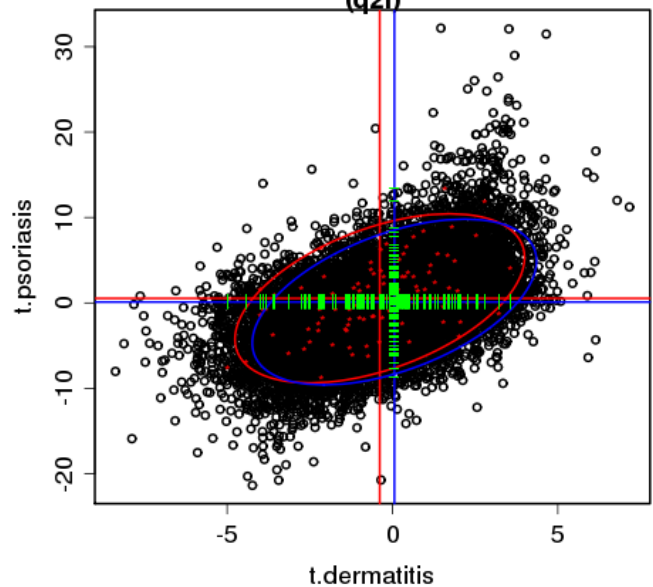
GO:0006512



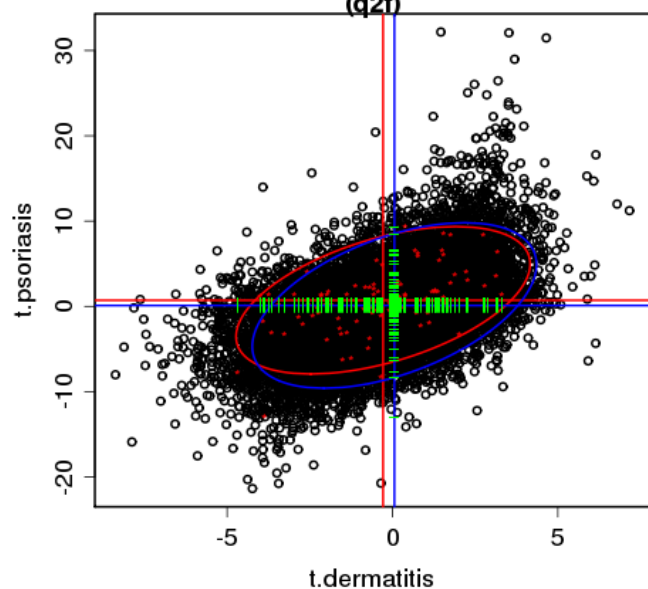
GO:0016567
protein ubiquitination
(q2f)



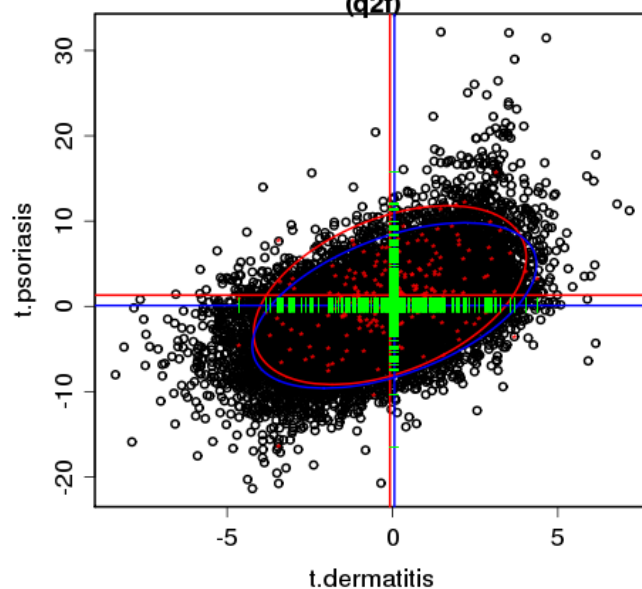
GO:0032446
protein modification by small protein conjugation
(q2f)



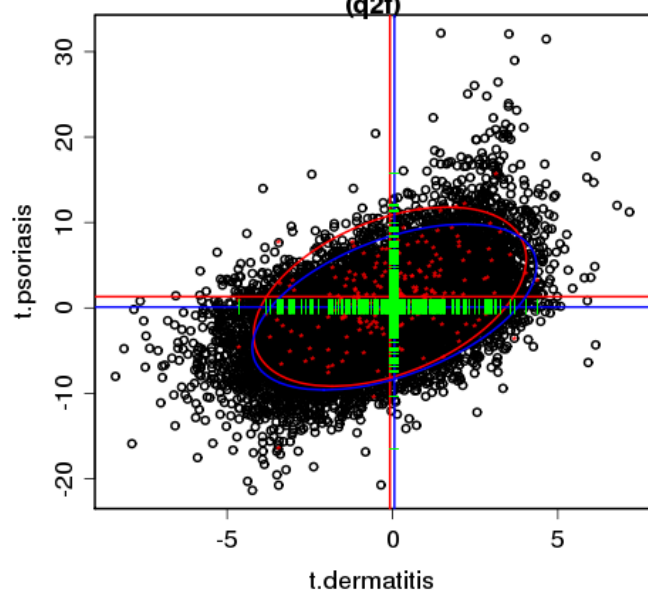
GO:0016125
sterol metabolic process
(q2f)



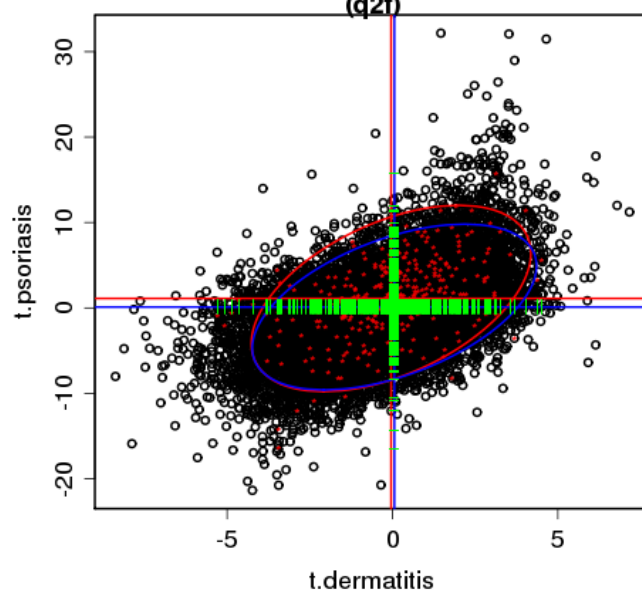
GO:0006913
nucleocytoplasmic transport
(q2f)



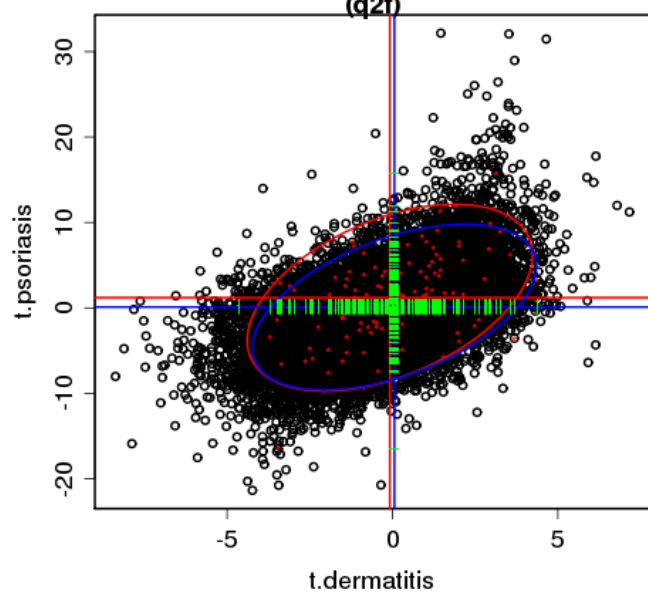
GO:0051169
nuclear transport
(q2f)



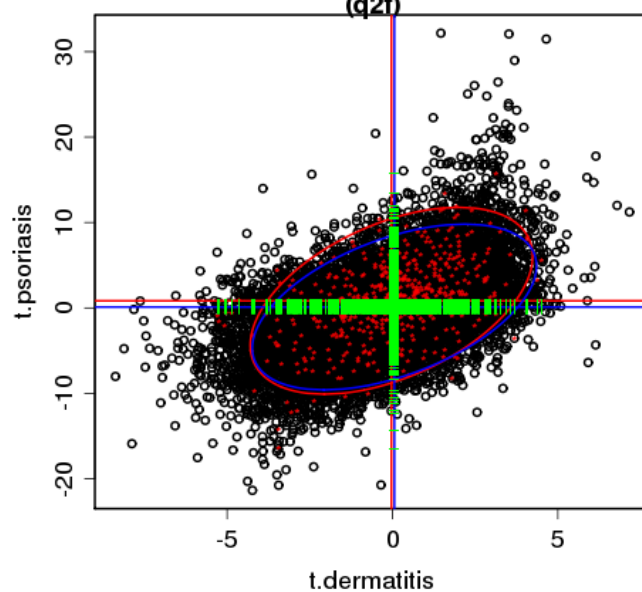
GO:0006605
protein targeting
(q2f)



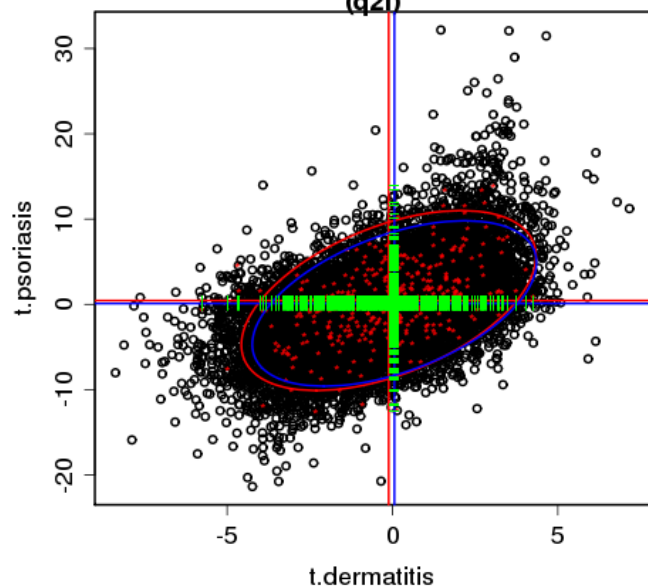
GO:0006606
protein import into nucleus
(q2f)



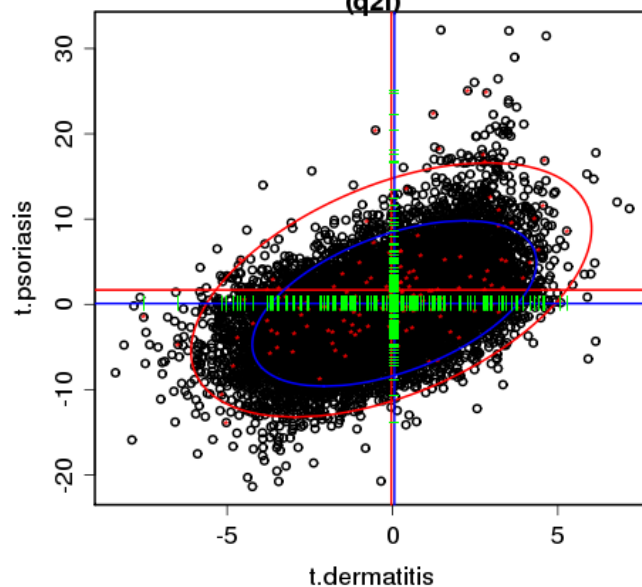
GO:0006886
intracellular protein transport
(q2f)



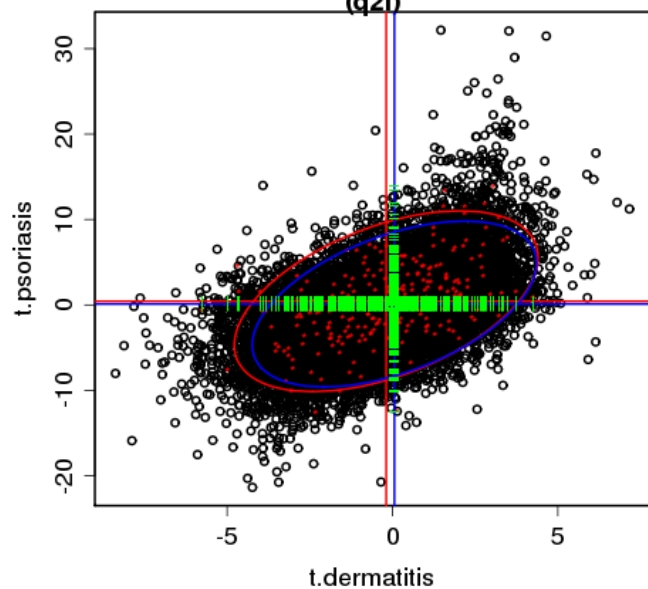
GO:0043285
biopolymer catabolic process
(q2f)



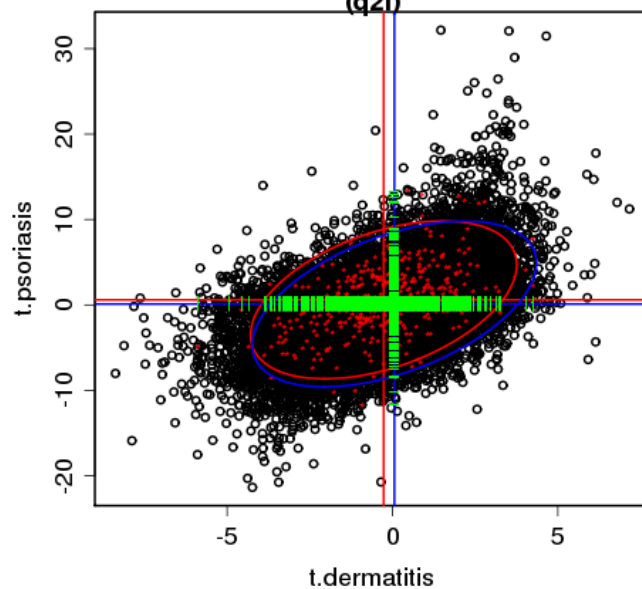
GO:0008544
epidermis development
(q2f)



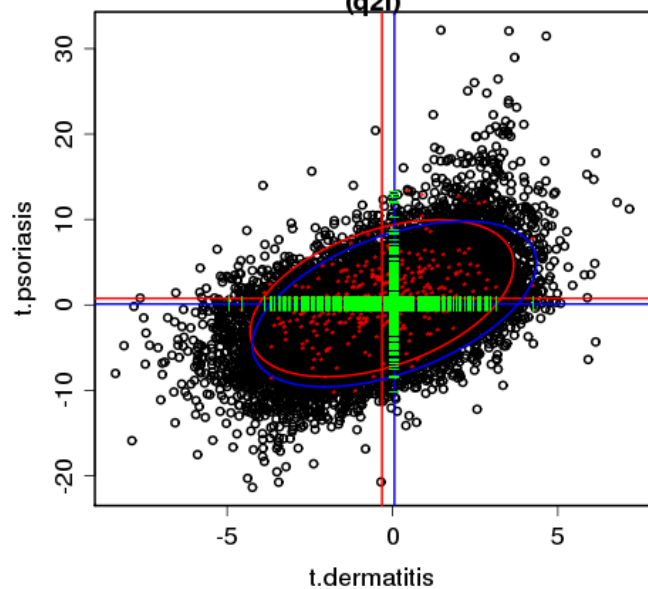
GO:0030163
protein catabolic process
(q2f)



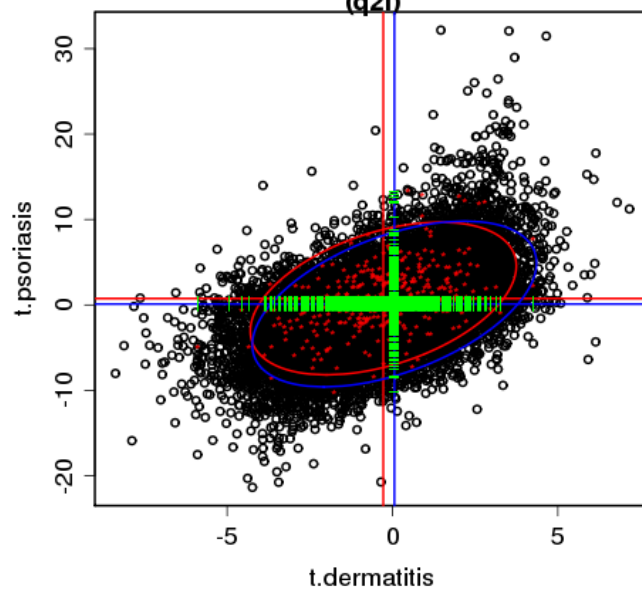
GO:0016071
mRNA metabolic process
(q2f)



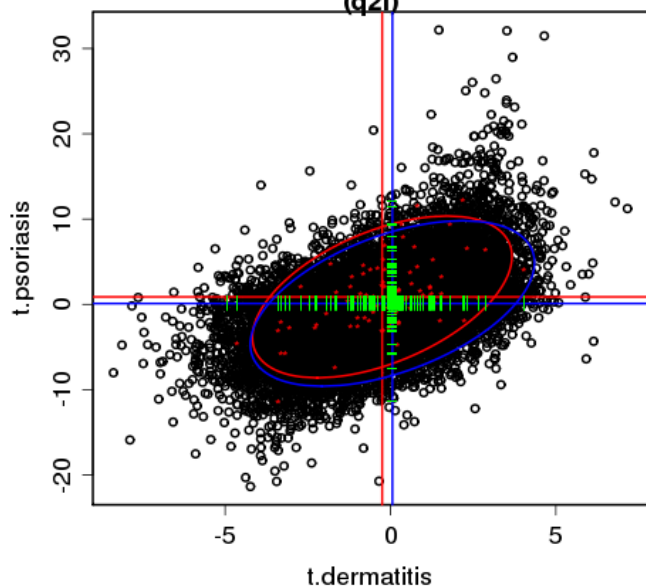
GO:0008380
RNA splicing
(q2f)



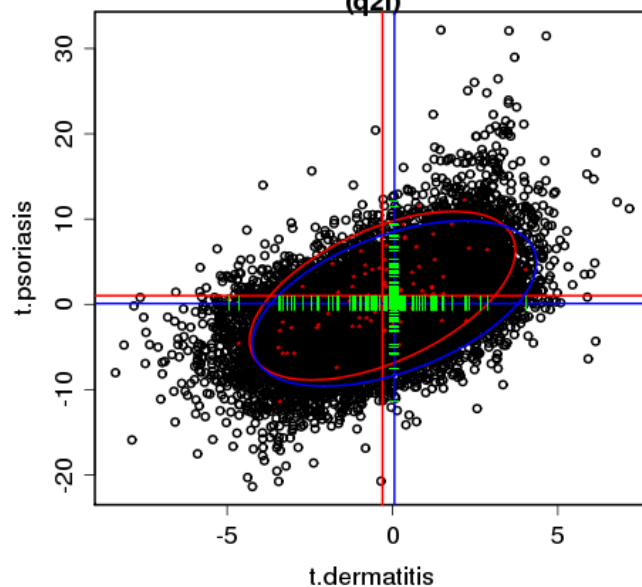
GO:0006397
mRNA processing
(q2f)



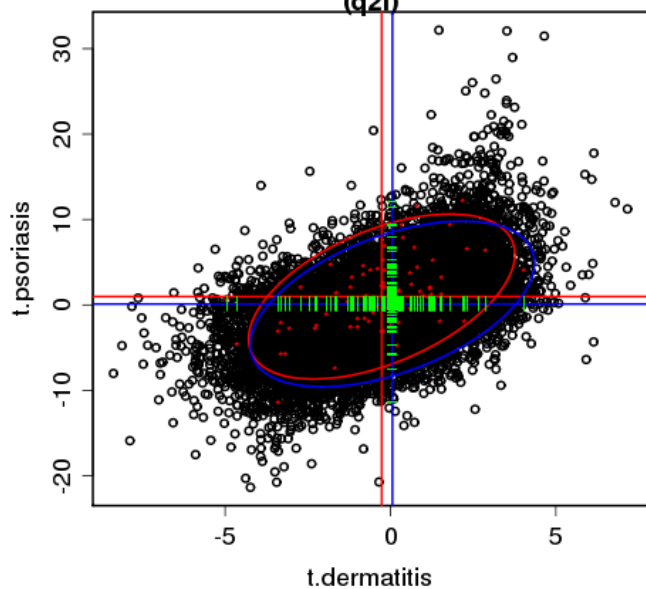
GO:0006403
RNA localization
(q2f)



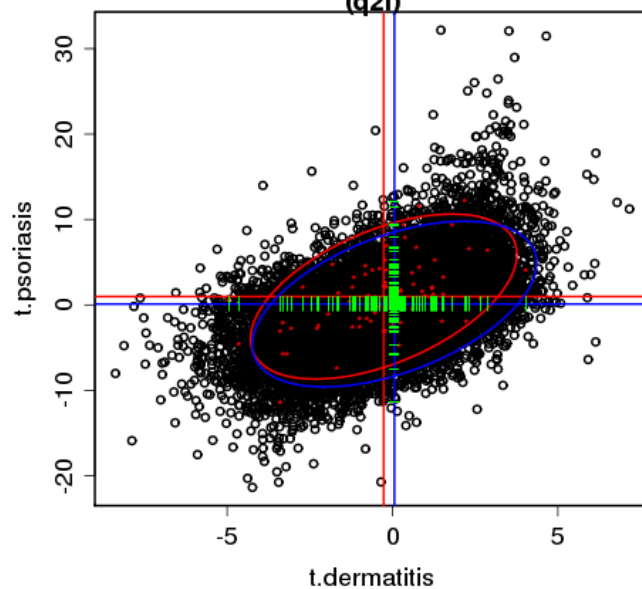
GO:0015931
nucleobase, nucleoside, nucleotide and nucleic acid transp
(q2f)



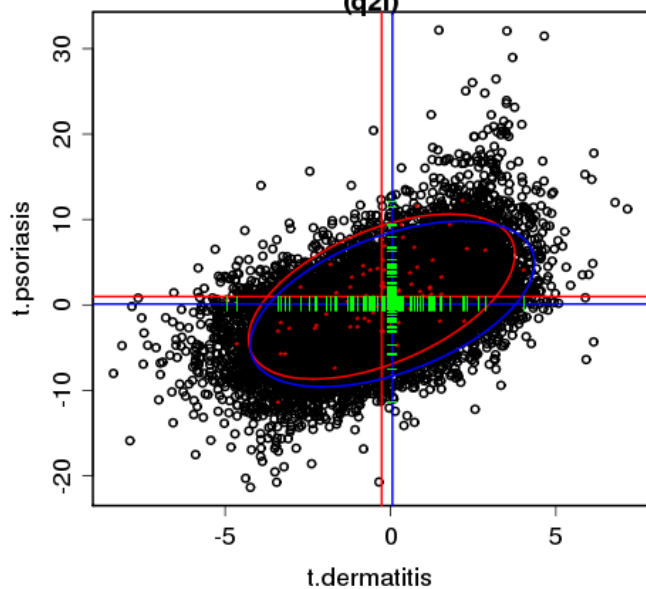
GO:0050657
nucleic acid transport
(q2f)



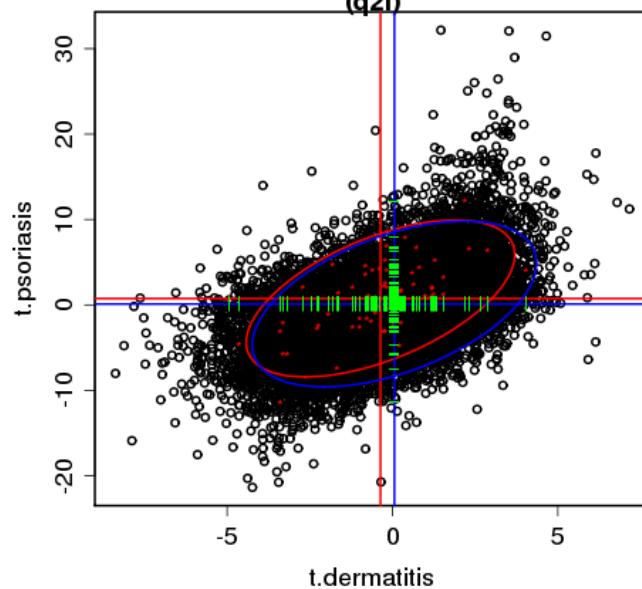
GO:0051236
establishment of RNA localization
(q2f)

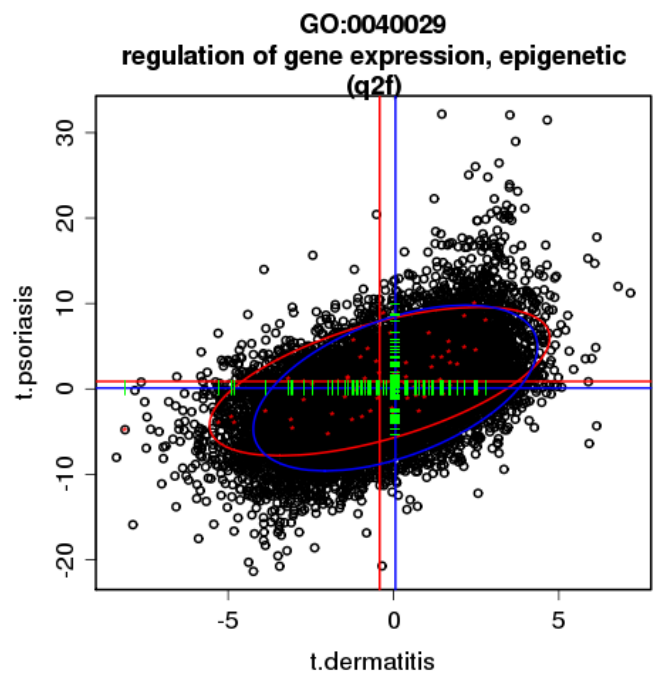
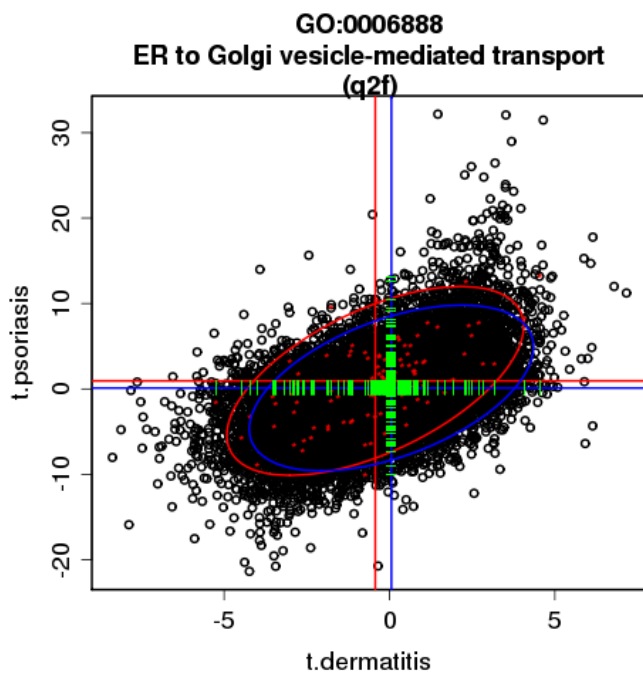
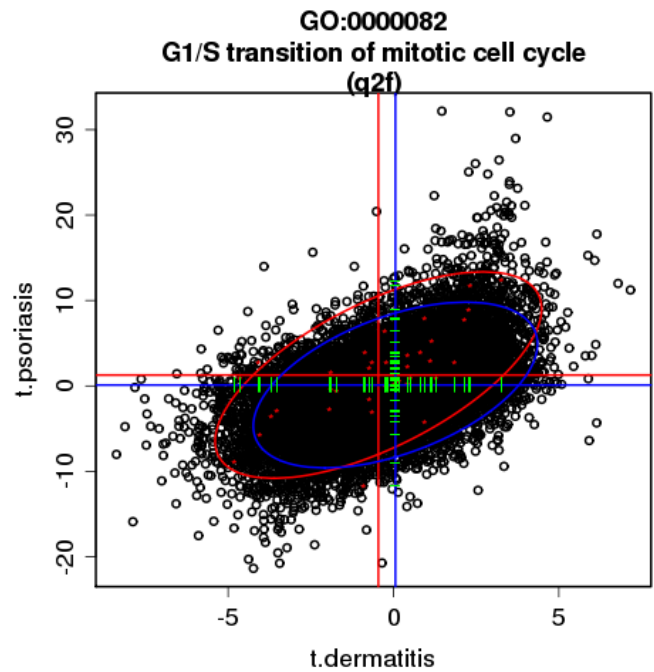
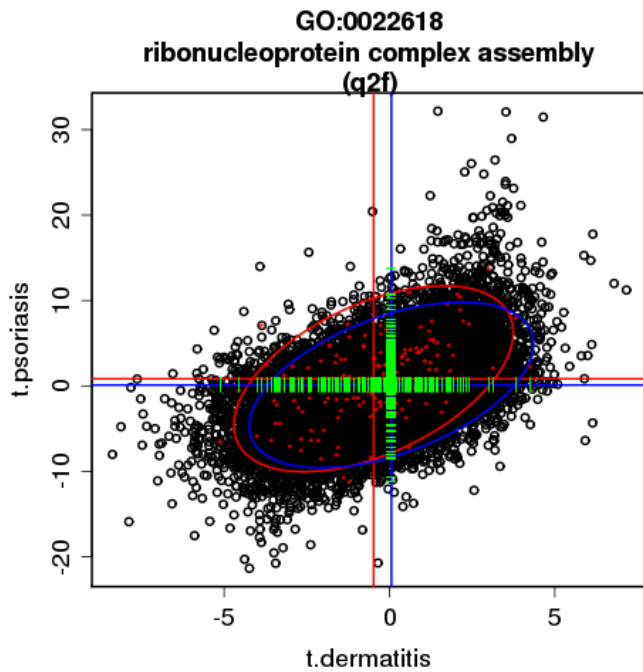
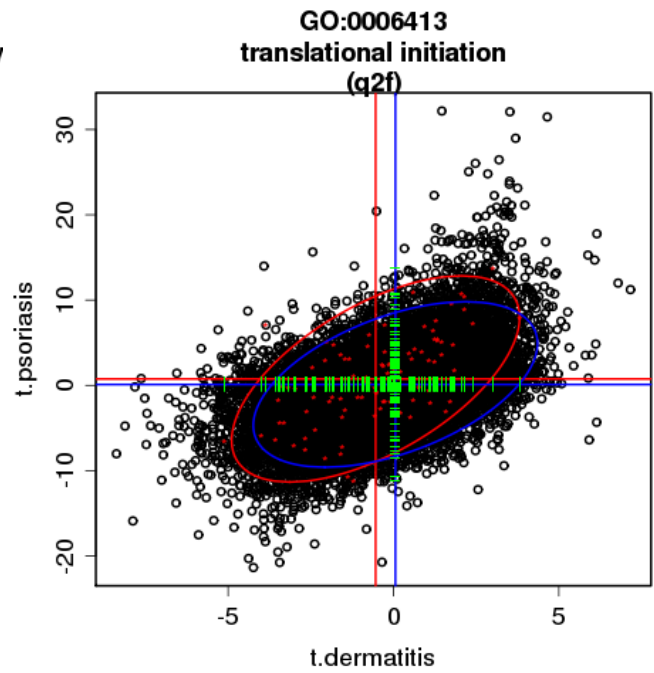
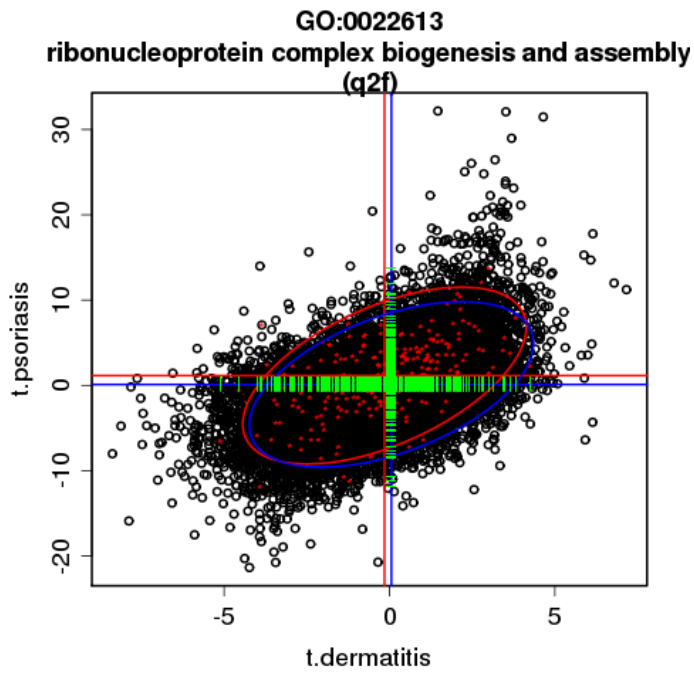


GO:0050658
RNA transport
(q2f)

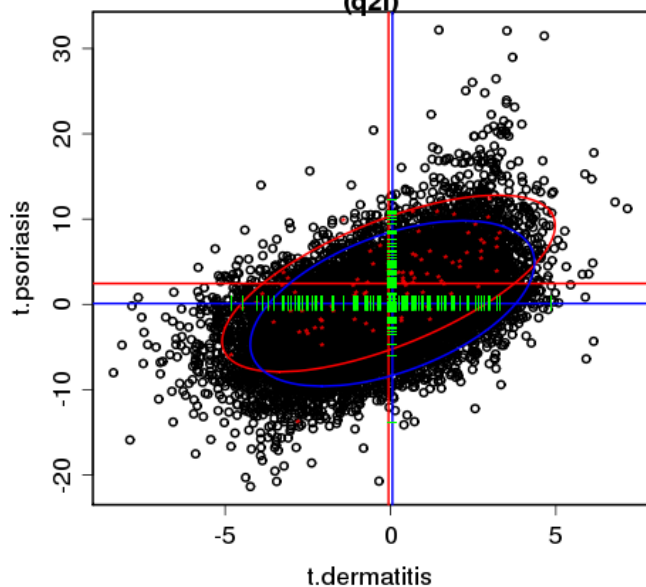


GO:0051028
mRNA transport
(q2f)

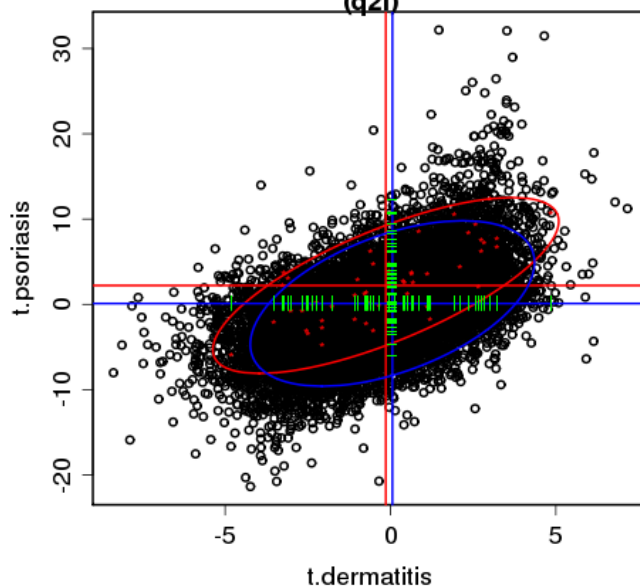




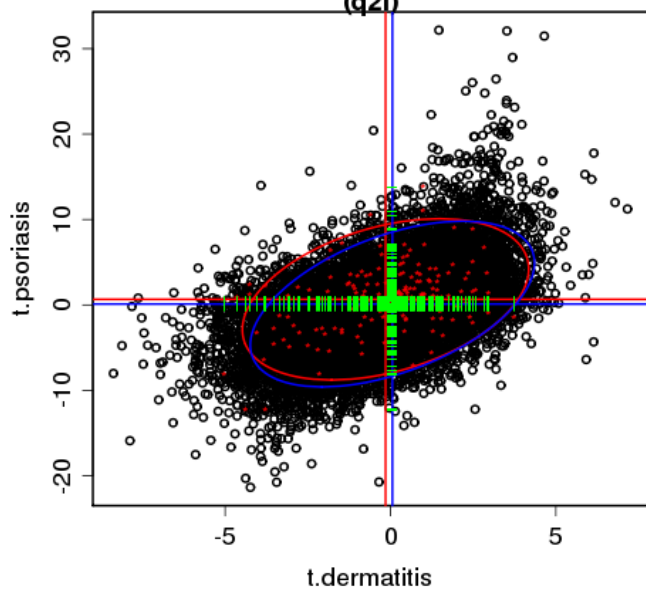
GO:0000075
cell cycle checkpoint
(q2f)



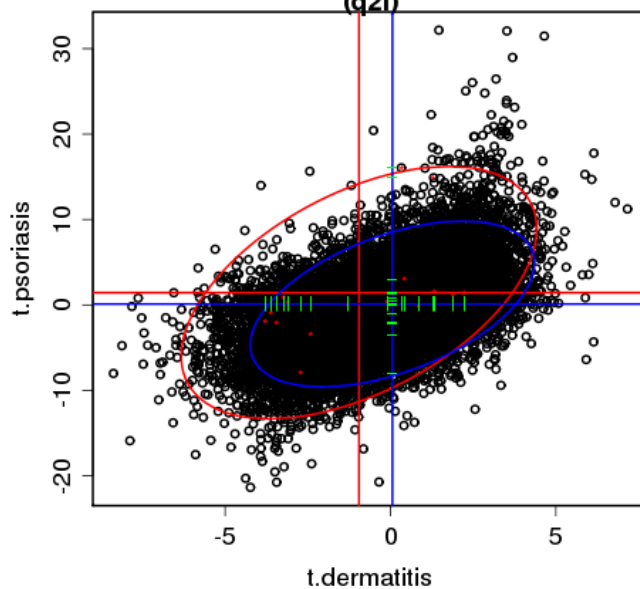
GO:0007093
mitotic cell cycle checkpoint
(q2f)



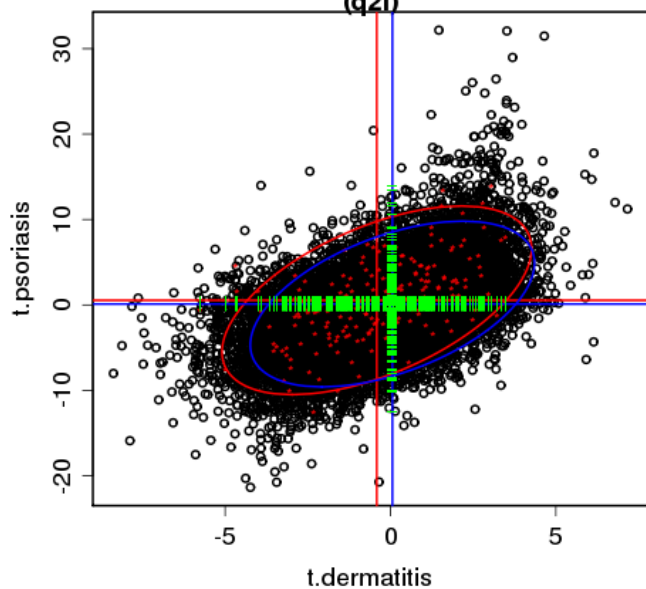
GO:0006470
protein amino acid dephosphorylation
(q2f)



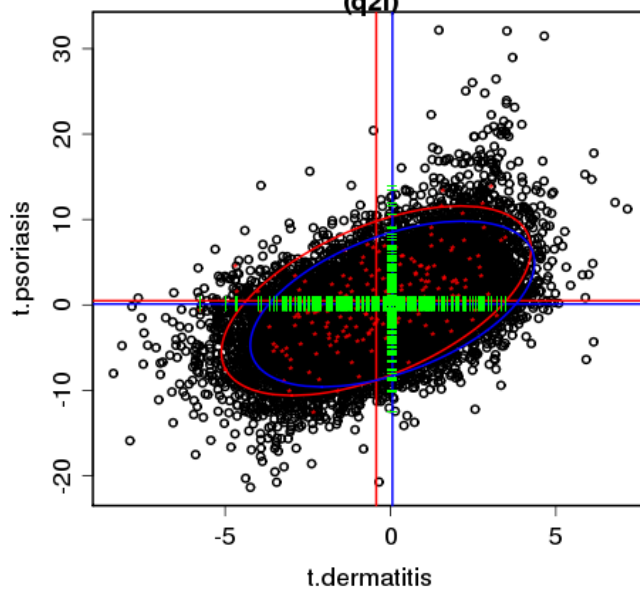
GO:0007567
parturition
(q2f)



GO:0044257
cellular protein catabolic process
(q2f)



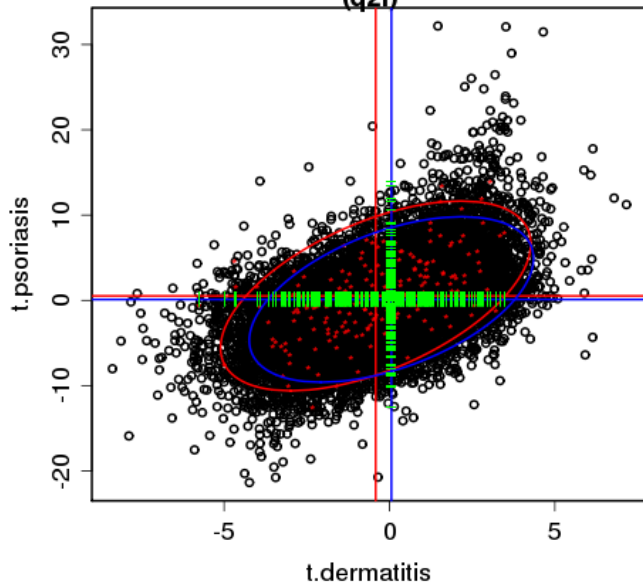
GO:0006511
ubiquitin-dependent protein catabolic process
(q2f)



GO:0019941

modification-dependent protein catabolic process

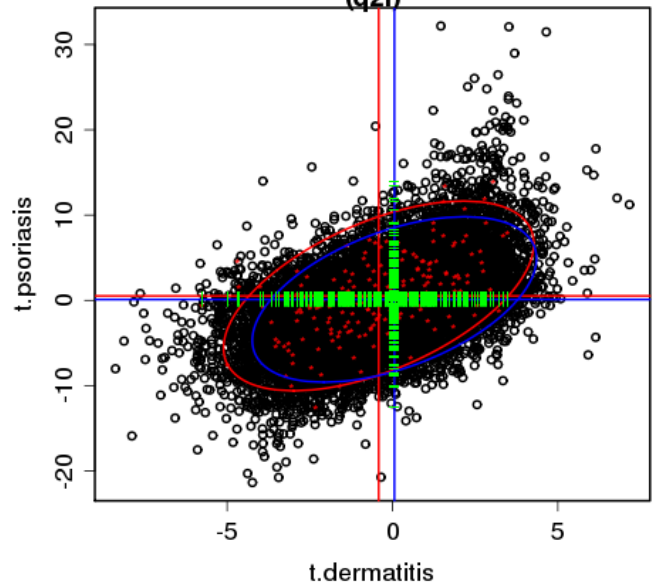
(q2f)



GO:0043632

modification-dependent macromolecule catabolic process

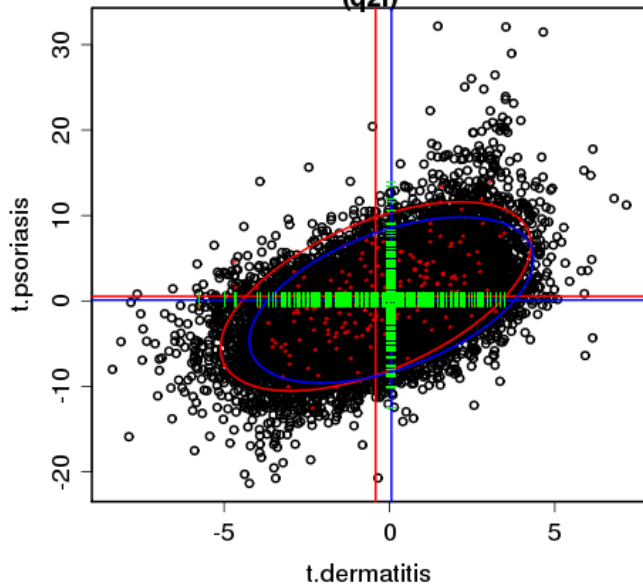
(q2f)



GO:0051603

proteolysis involved in cellular protein catabolic process

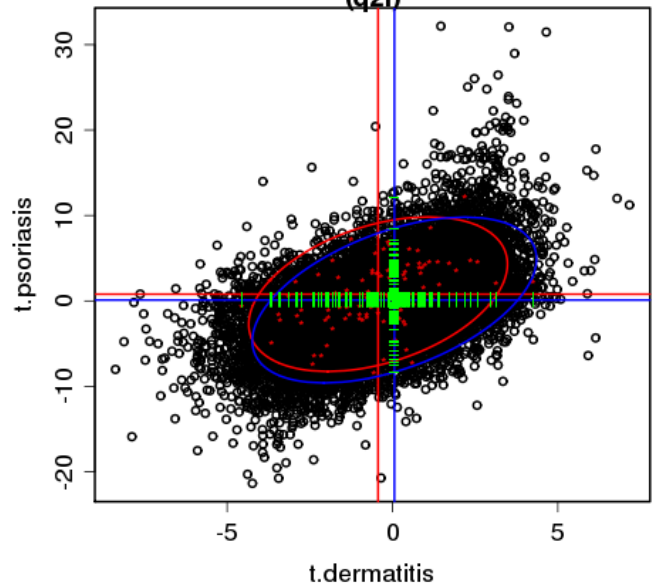
(q2f)



GO:0000375

RNA splicing, via transesterification reactions

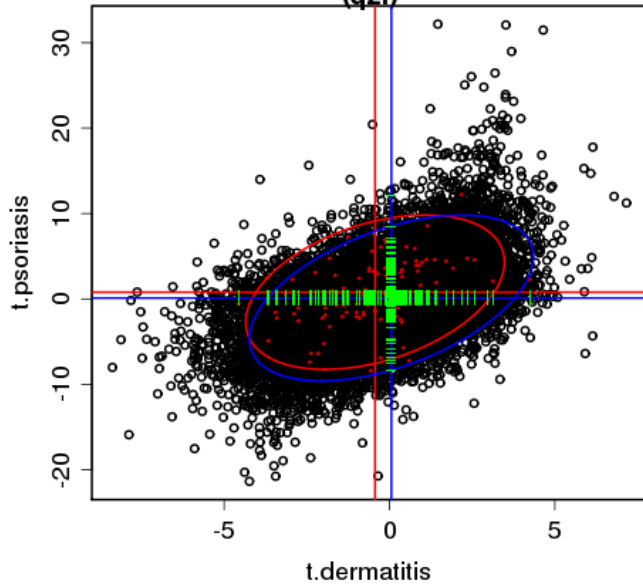
(q2f)



GO:0000377

RNA splicing, via transesterification reactions with bulged adenosine

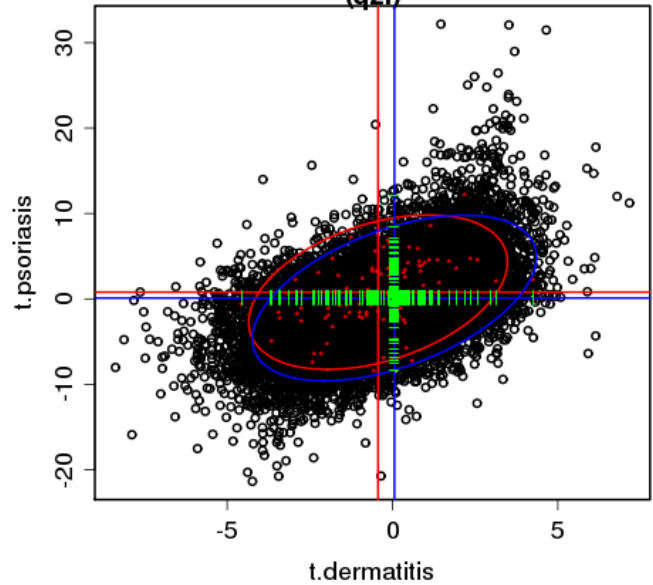
(q2f)



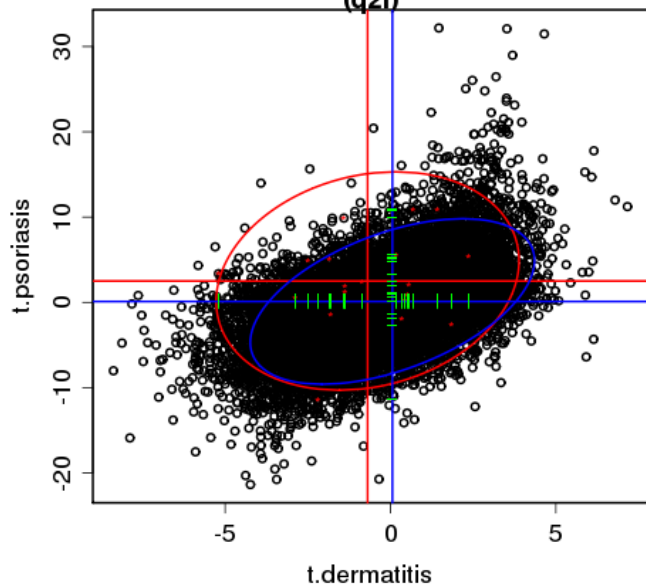
GO:0000398

nuclear mRNA splicing, via spliceosome

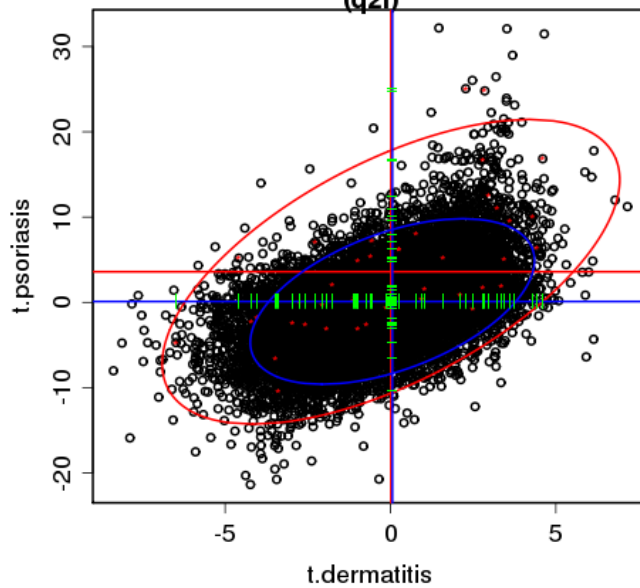
(q2f)



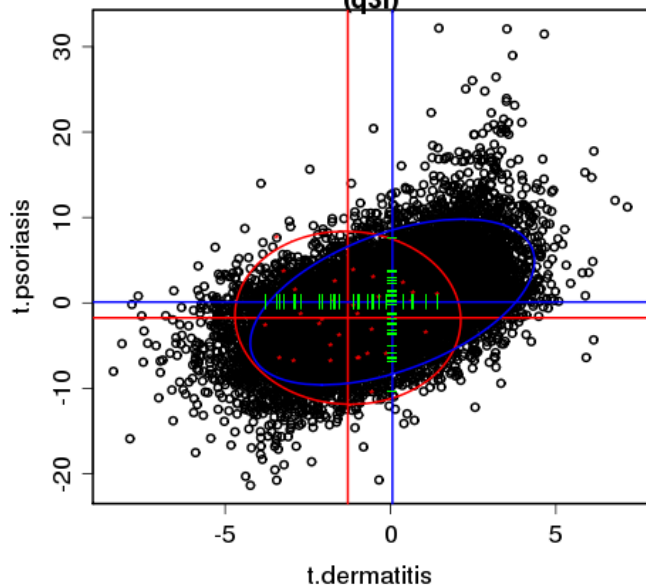
GO:0045646
regulation of erythrocyte differentiation
(q2f)



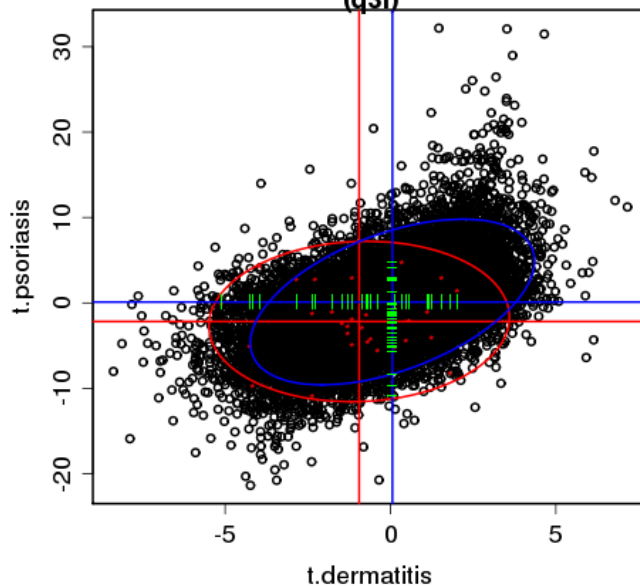
GO:0030216
keratinocyte differentiation
(q2f)



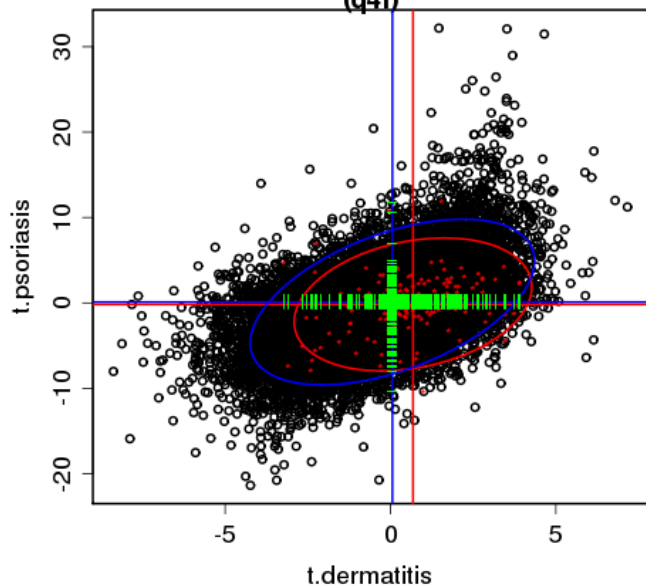
GO:0016573
histone acetylation
(q3f)



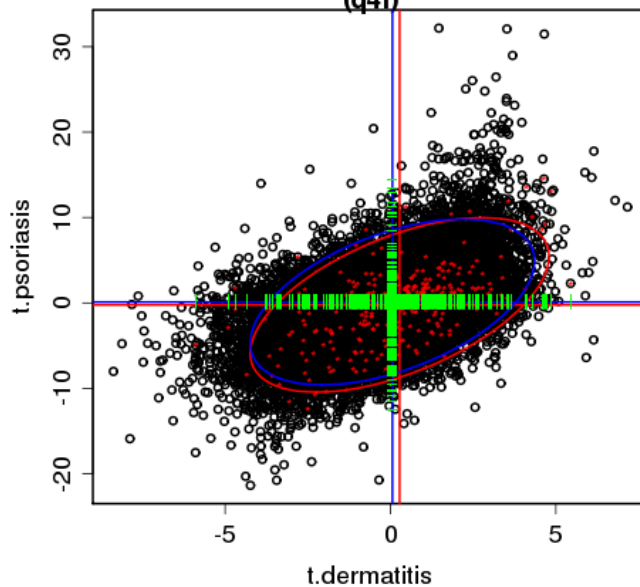
GO:0006892
post-Golgi vesicle-mediated transport
(q3f)

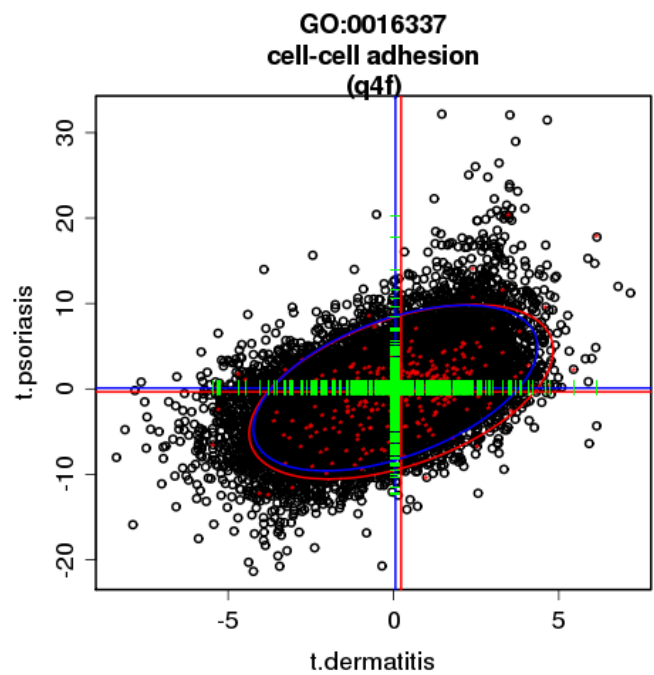
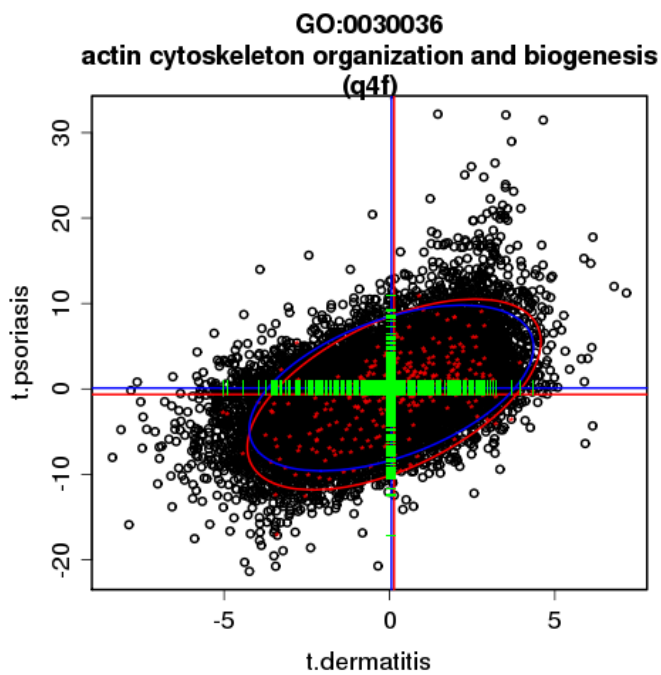
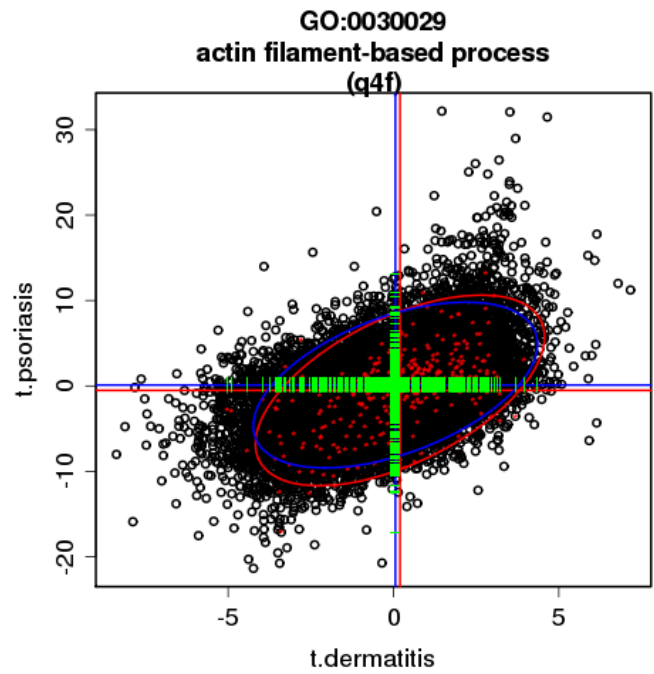
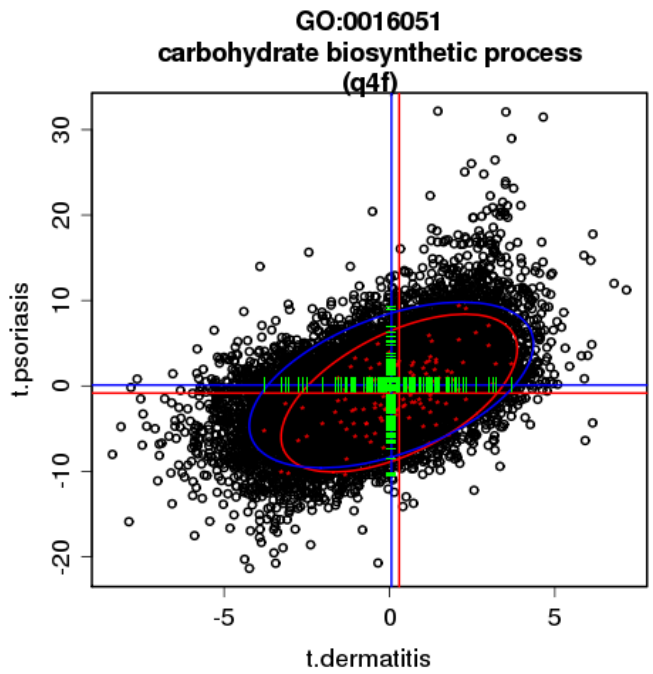
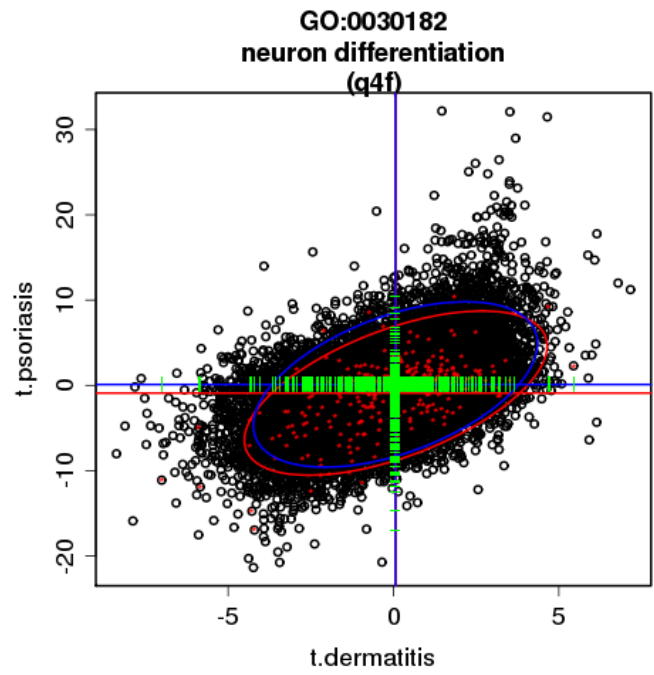
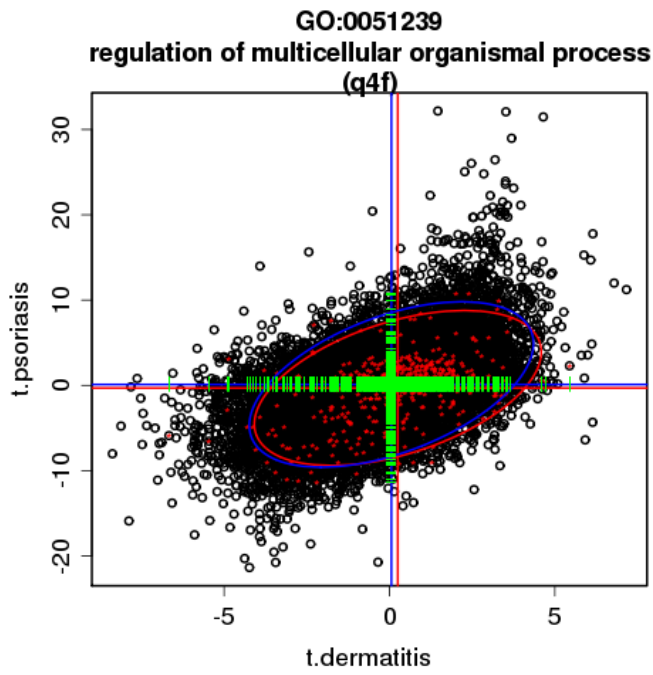


GO:0015698
inorganic anion transport
(q4f)



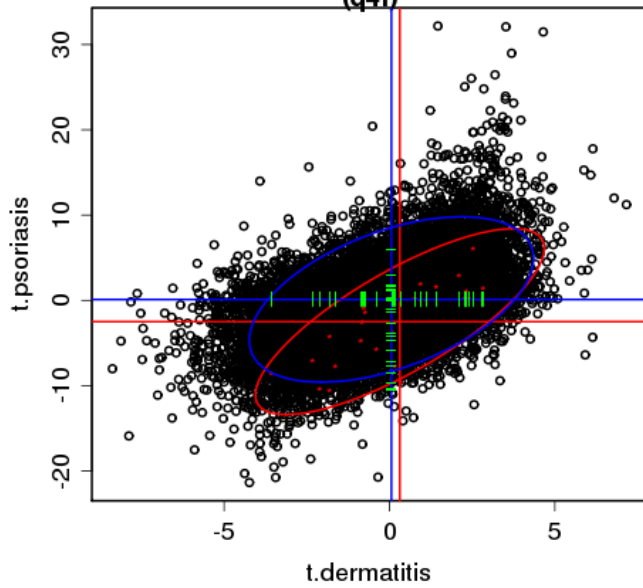
GO:0016477
cell migration
(q4f)





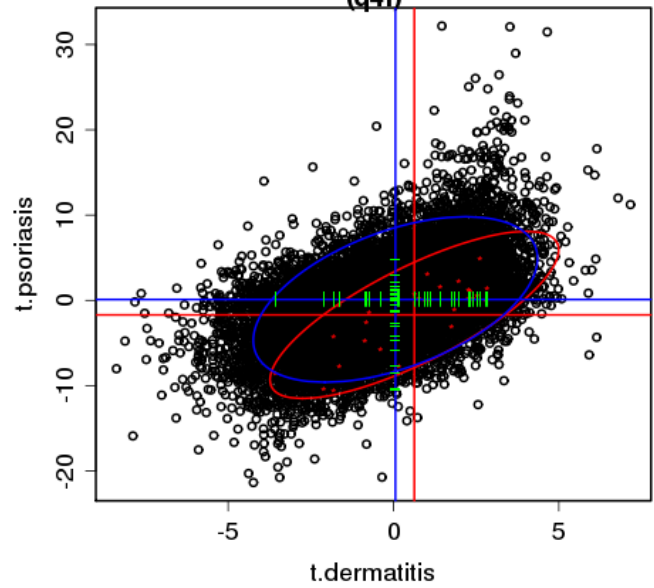
GO:0031032

actomyosin structure organization and biogenesis
(q4f)



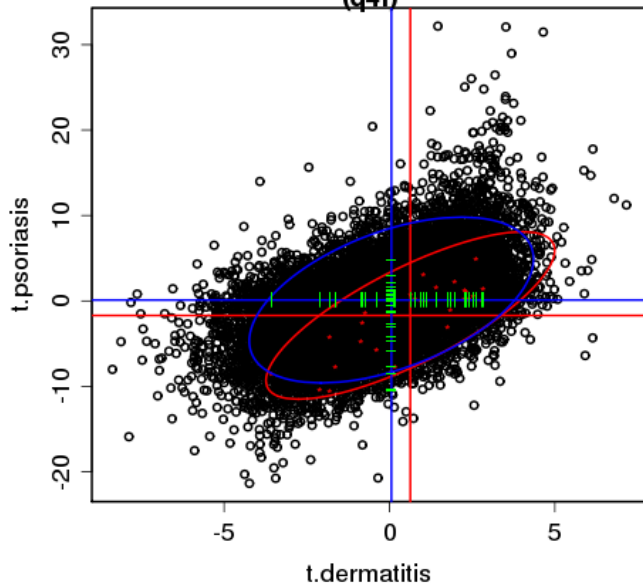
GO:0048627

myoblast development
(q4f)



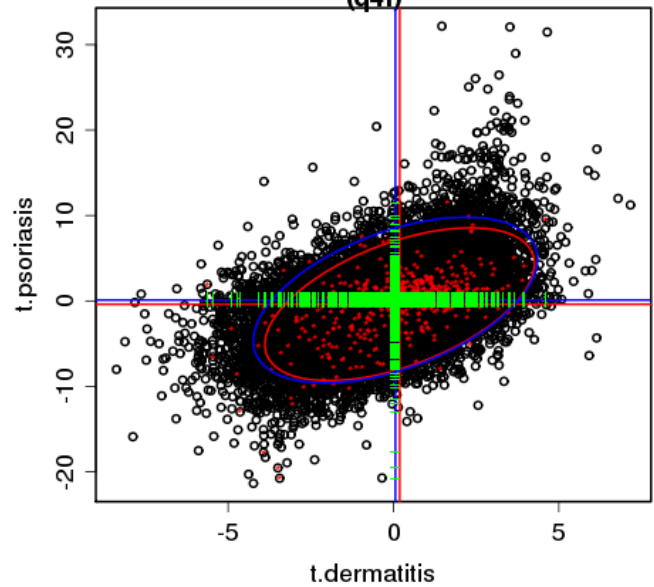
GO:0048628

myoblast maturation
(q4f)



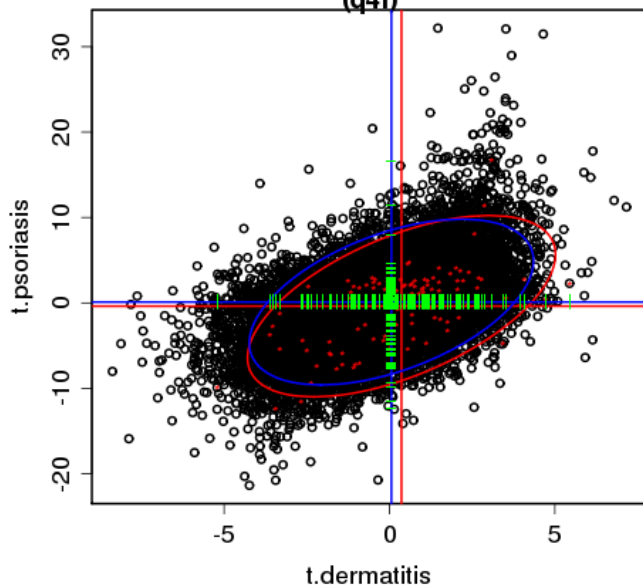
GO:0007600

sensory perception
(q4f)



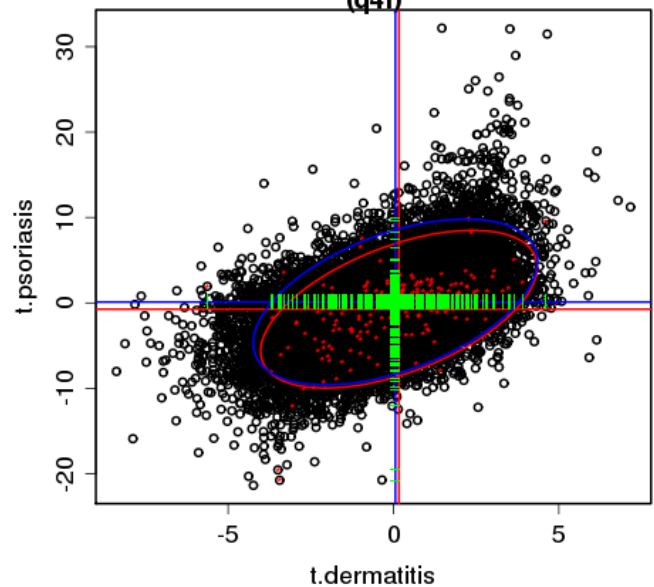
GO:0031589

cell-substrate adhesion
(q4f)

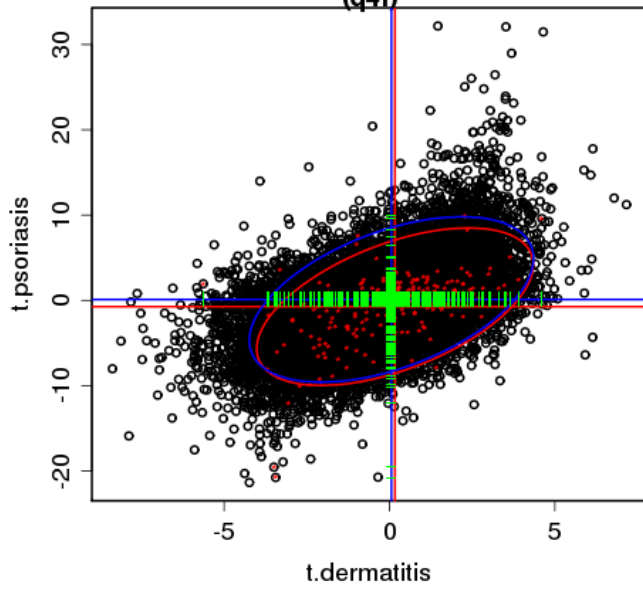


GO:0050953

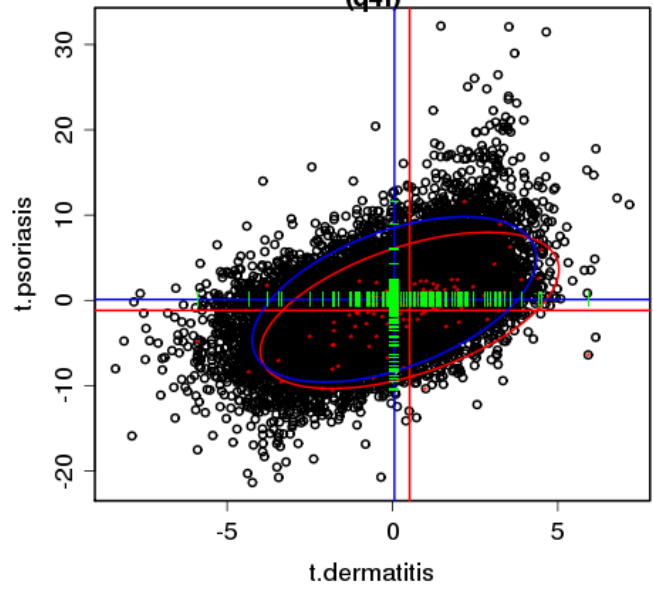
sensory perception of light stimulus
(q4f)



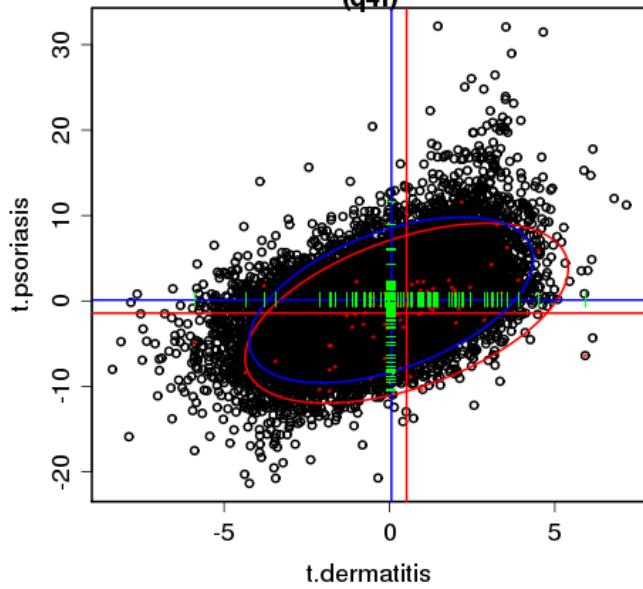
GO:0007601
visual perception
(q4f)



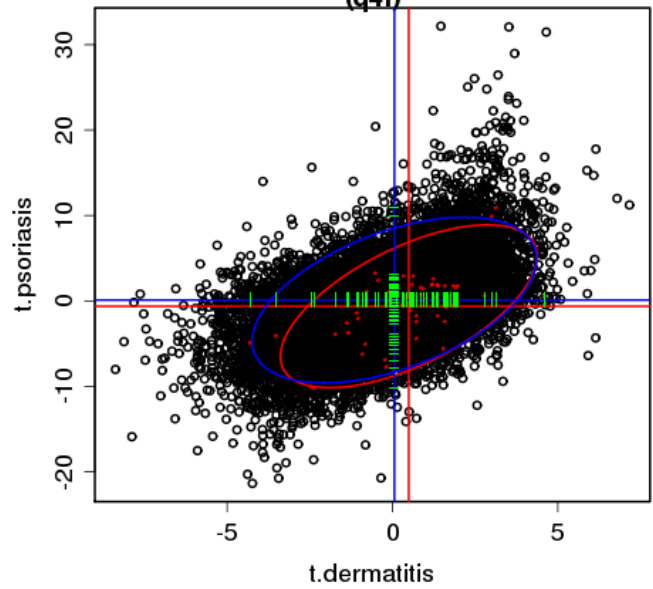
GO:0043062
extracellular structure organization and biogenesis
(q4f)



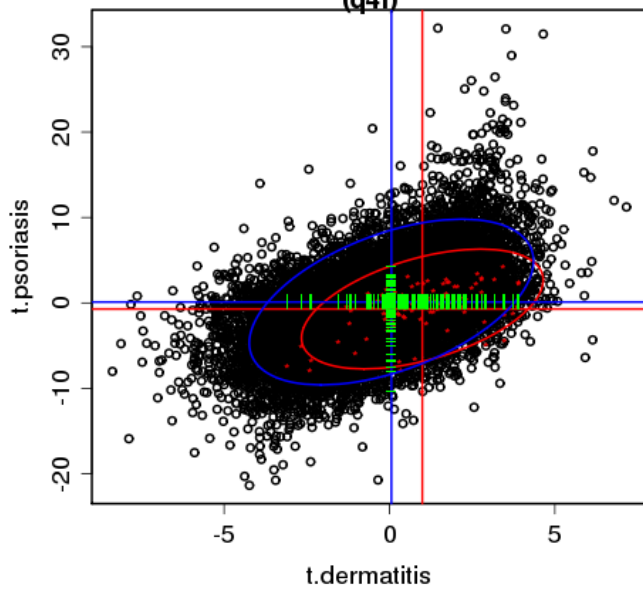
GO:0030198
extracellular matrix organization and biogenesis
(q4f)



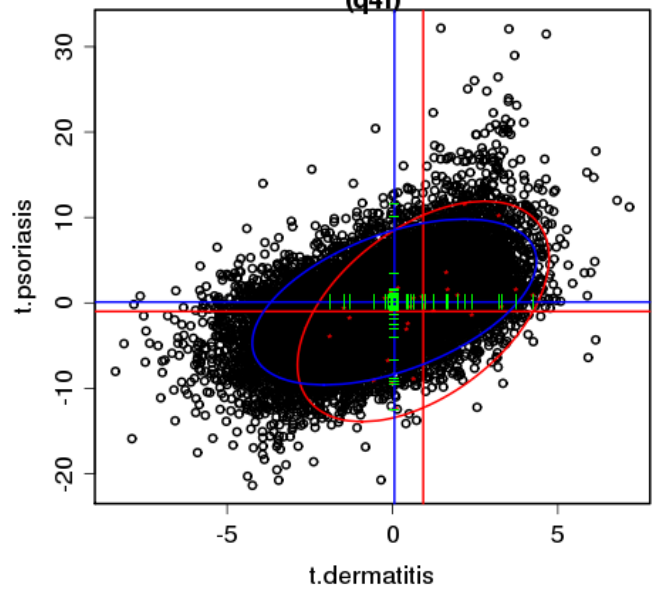
GO:0051046
regulation of secretion
(q4f)

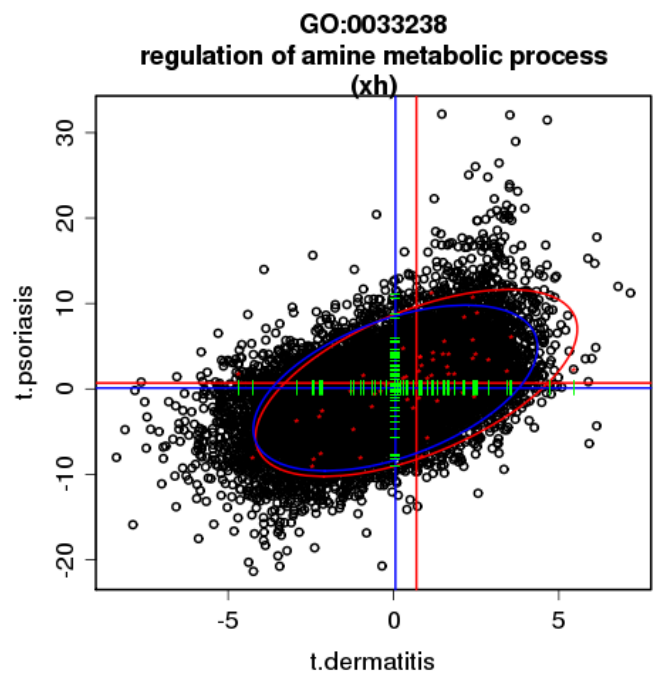
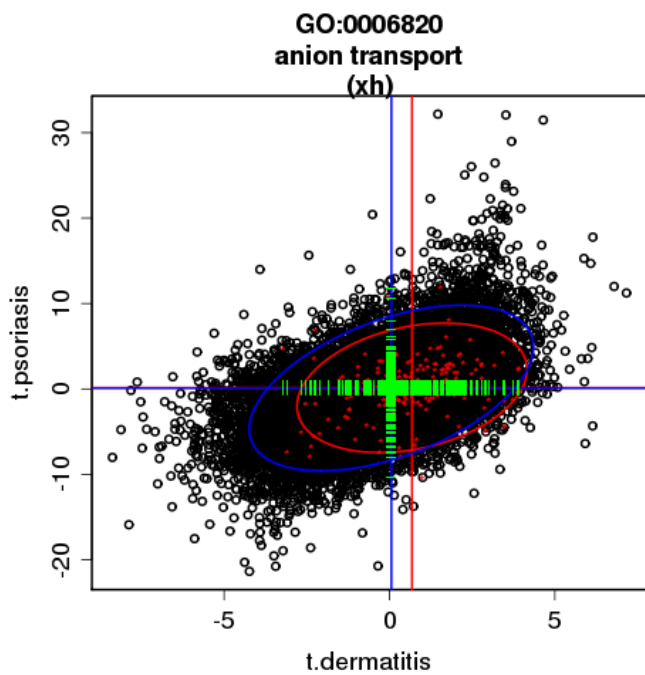
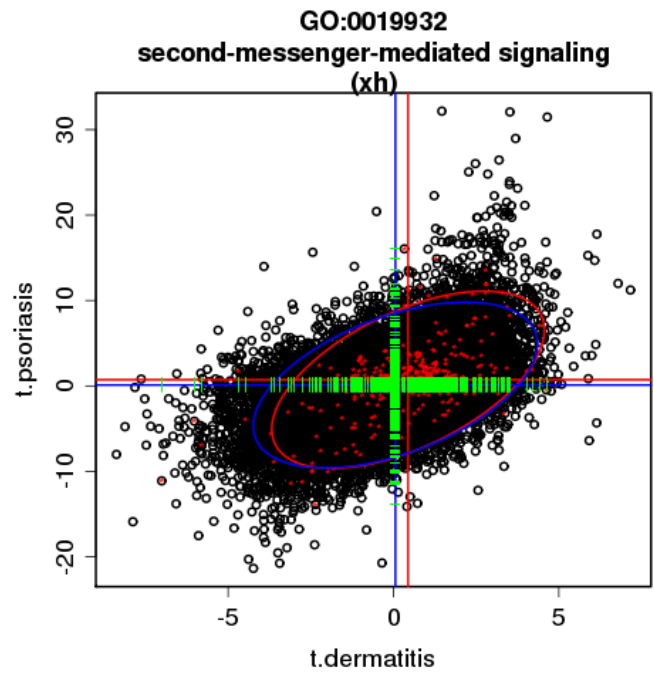
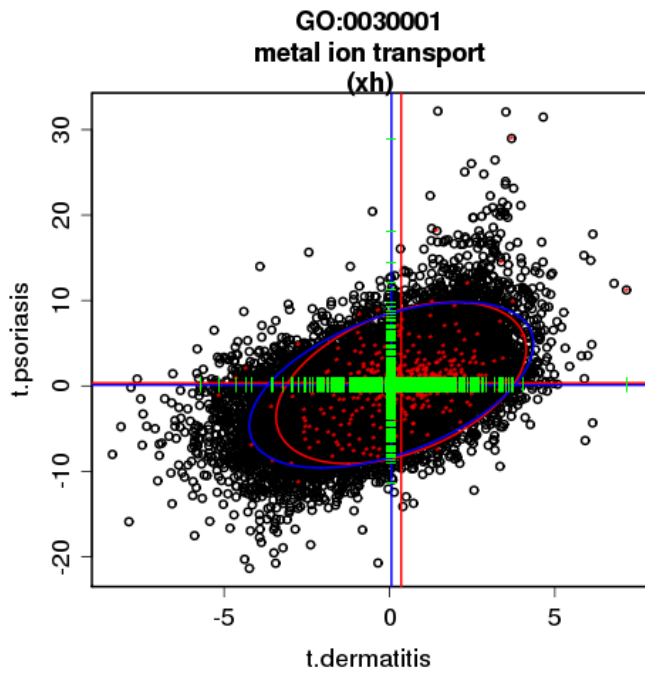
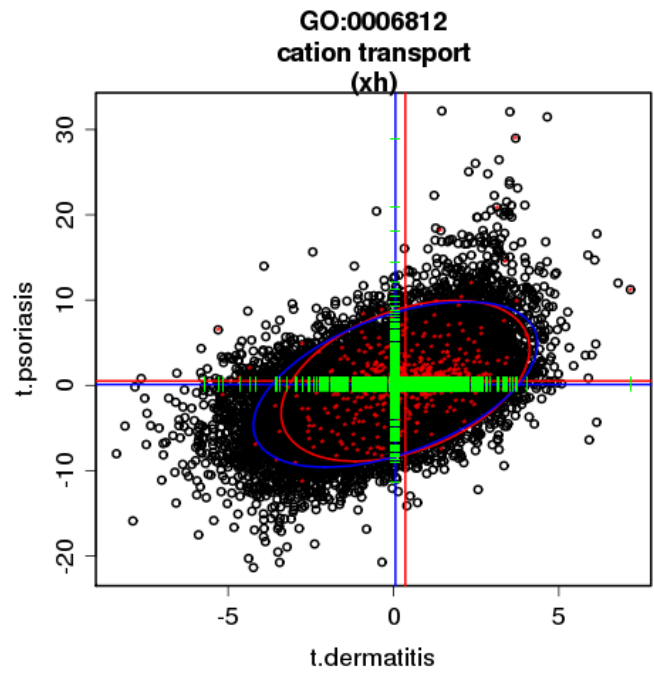
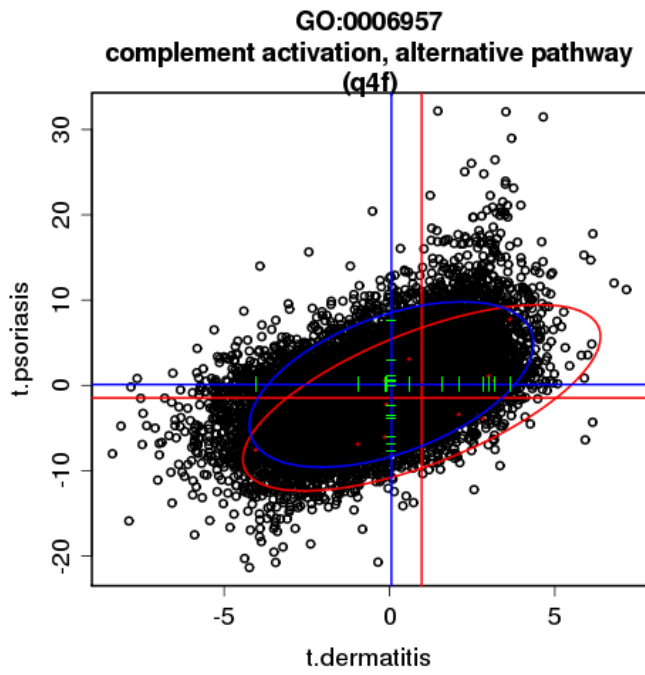


GO:0006817
phosphate transport
(q4f)



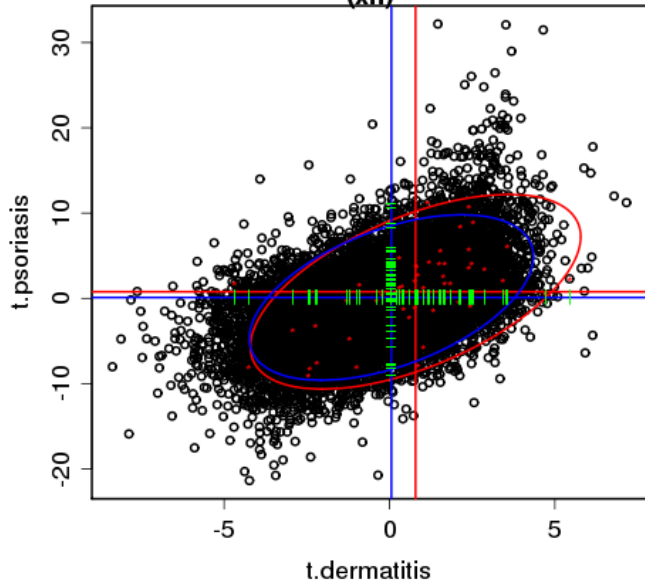
GO:0032963
collagen metabolic process
(q4f)





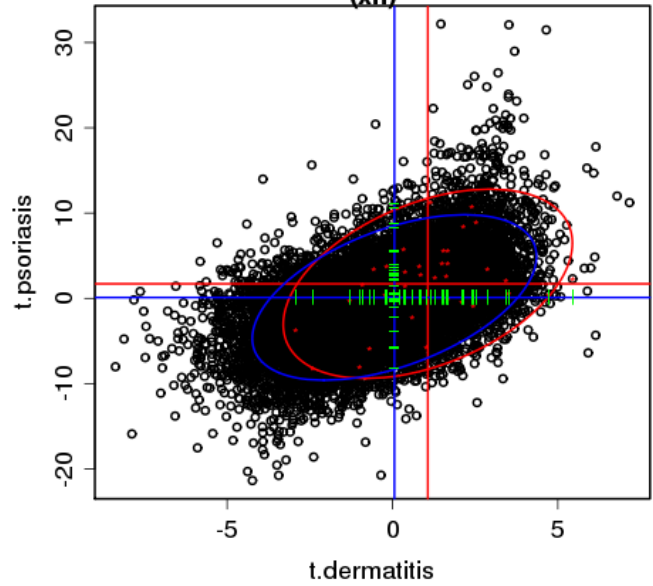
GO:0001932

regulation of protein amino acid phosphorylation
(xh)



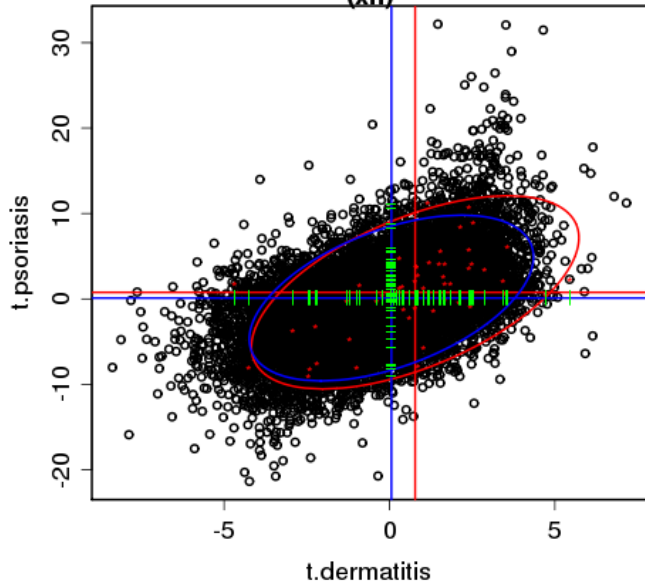
GO:0031401

positive regulation of protein modification process
(xh)



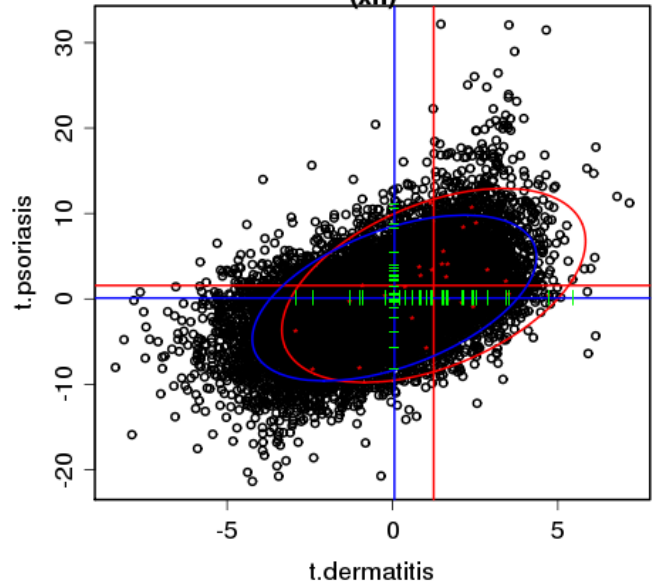
GO:0006521

regulation of amino acid metabolic process
(xh)



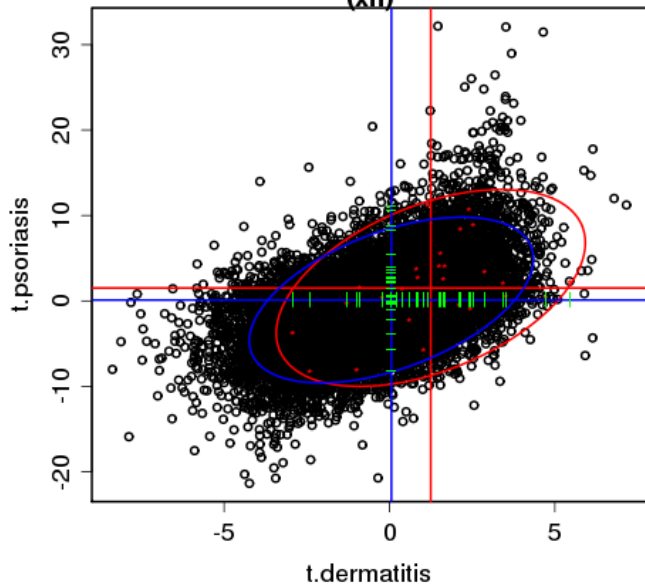
GO:0033240

positive regulation of amine metabolic process
(xh)



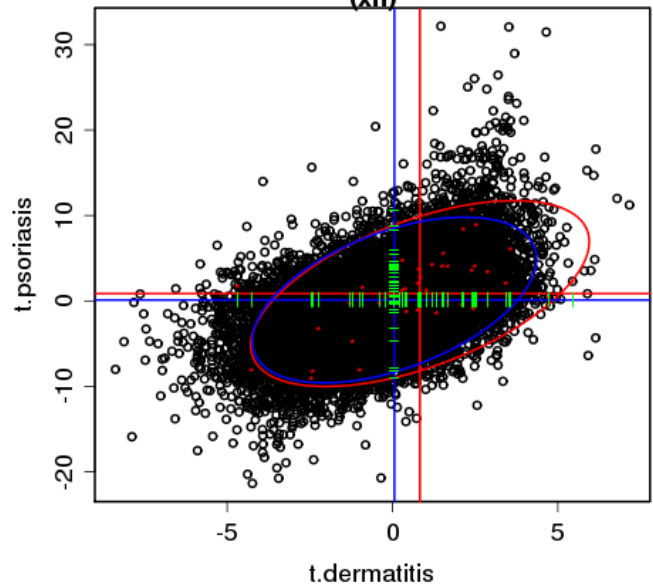
GO:0001934

positive regulation of protein amino acid phosphorylation
(xh)



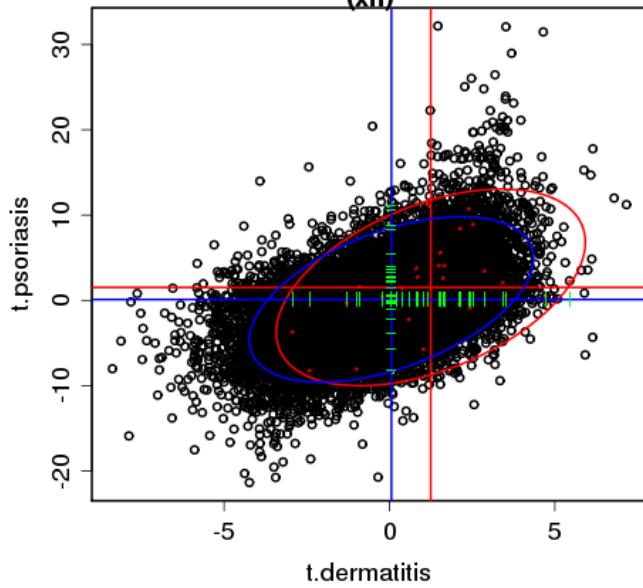
GO:0050730

regulation of peptidyl-tyrosine phosphorylation
(xh)



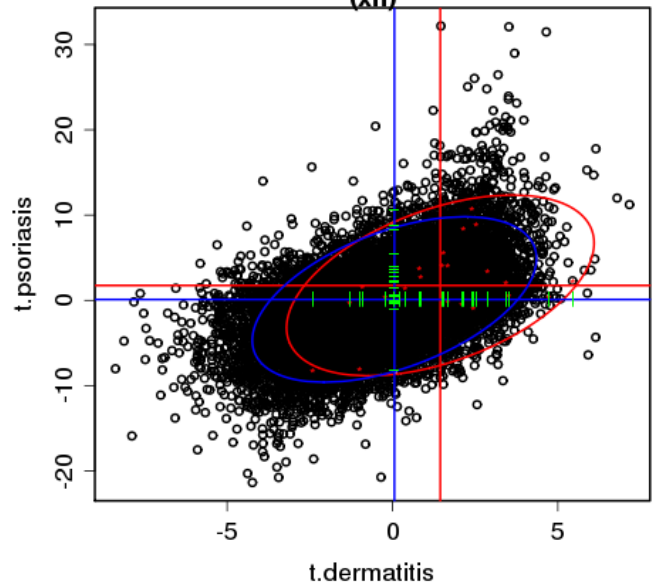
GO:0045764

positive regulation of amino acid metabolic process
(xh)



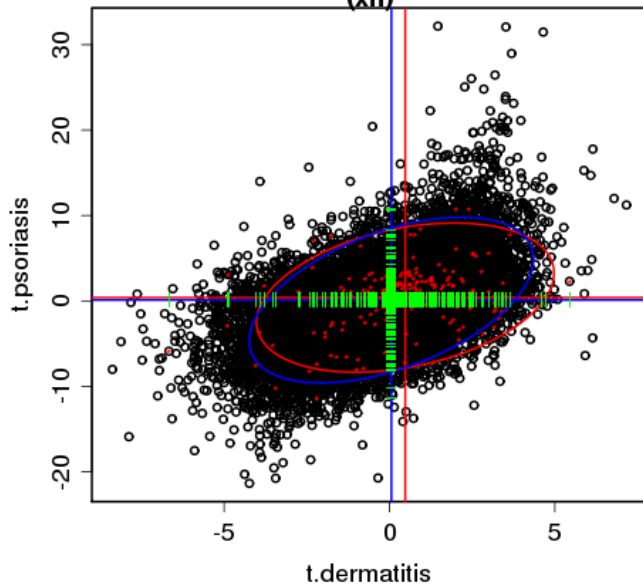
GO:0050731

positive regulation of peptidyl-tyrosine phosphorylation
(xh)



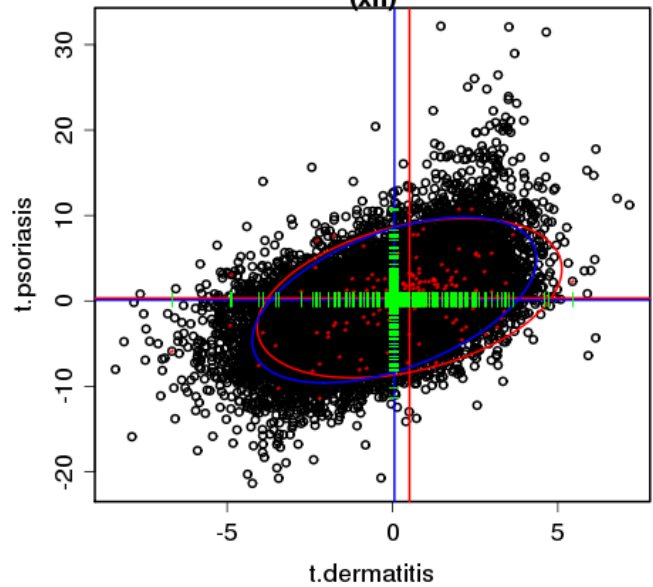
GO:0002682

regulation of immune system process
(xh)



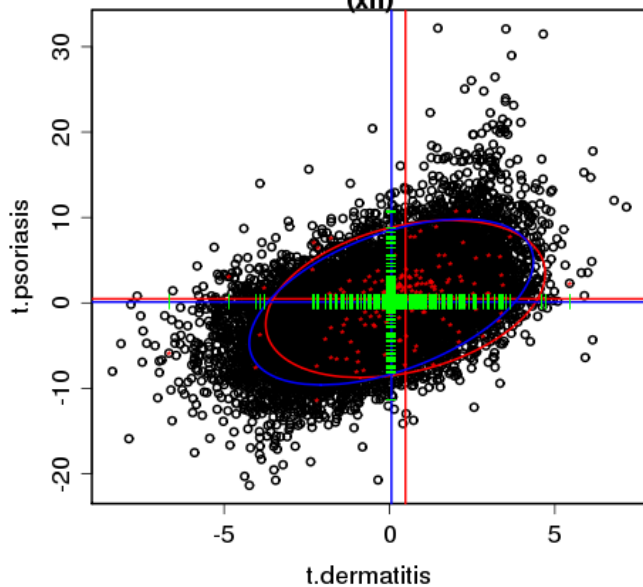
GO:0002684

positive regulation of immune system process
(xh)



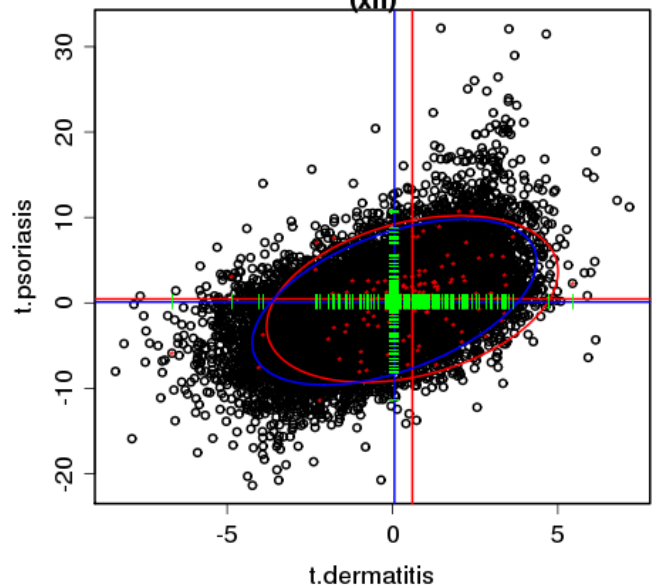
GO:0048583

regulation of response to stimulus
(xh)

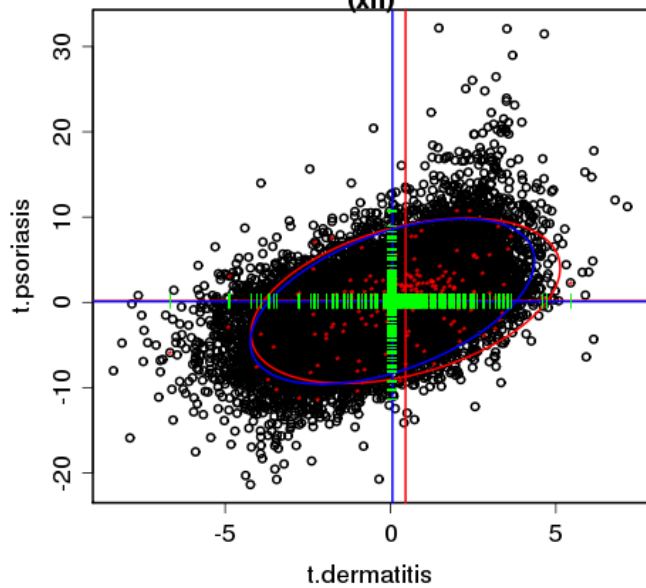


GO:0048584

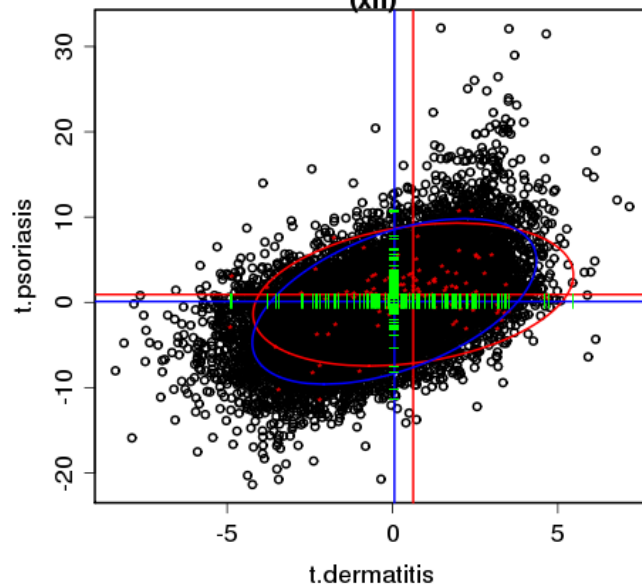
positive regulation of response to stimulus
(xh)



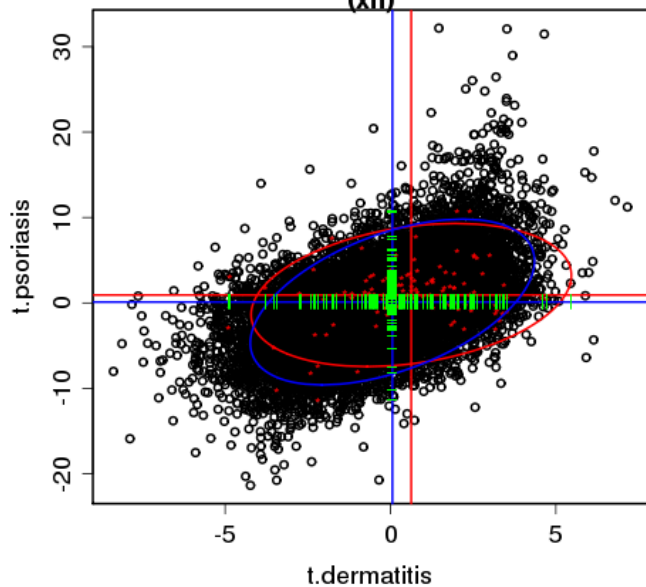
GO:0051240
positive regulation of multicellular organismal processes (xh)



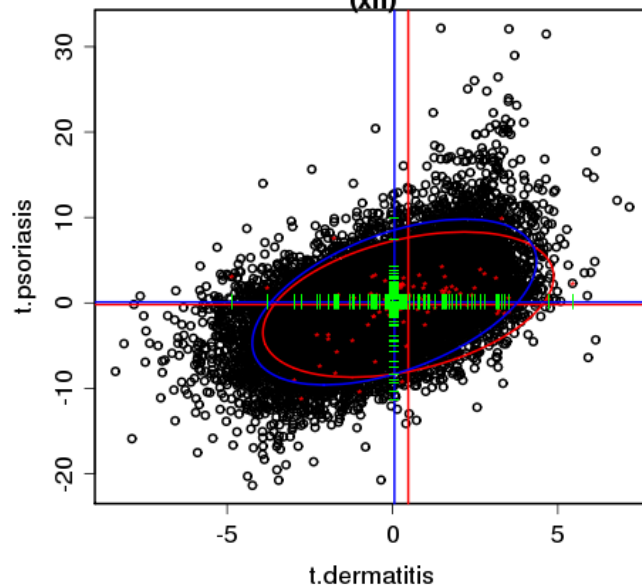
GO:0002694
regulation of leukocyte activation (xh)



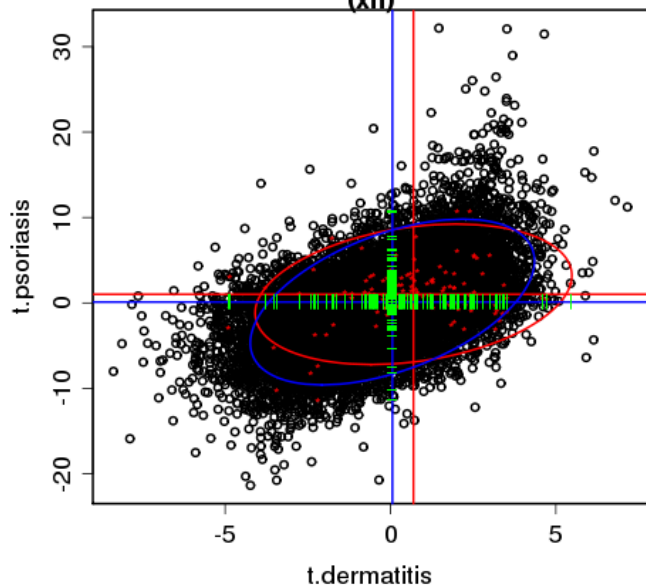
GO:0050865
regulation of cell activation (xh)



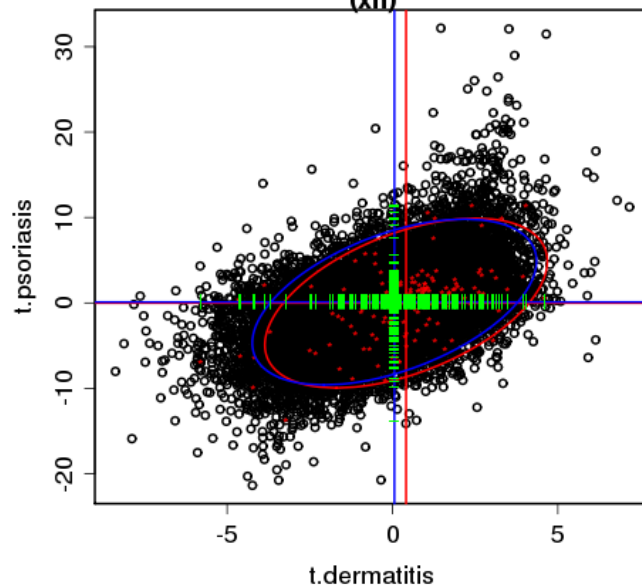
GO:0051241
negative regulation of multicellular organismal processes (xh)



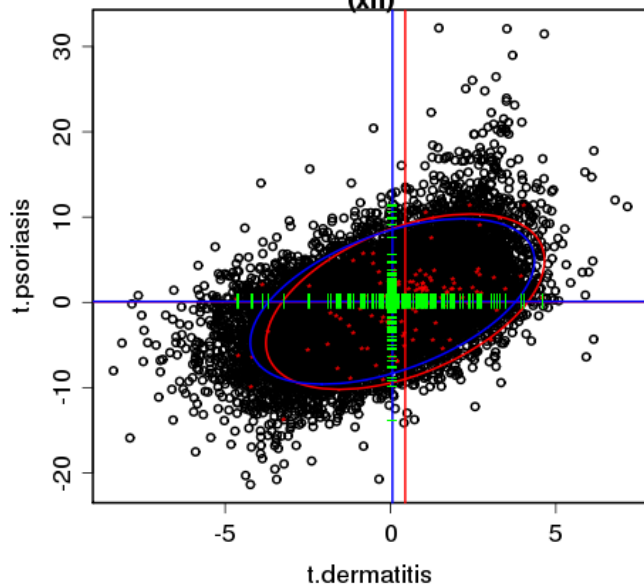
GO:0051249
regulation of lymphocyte activation (xh)



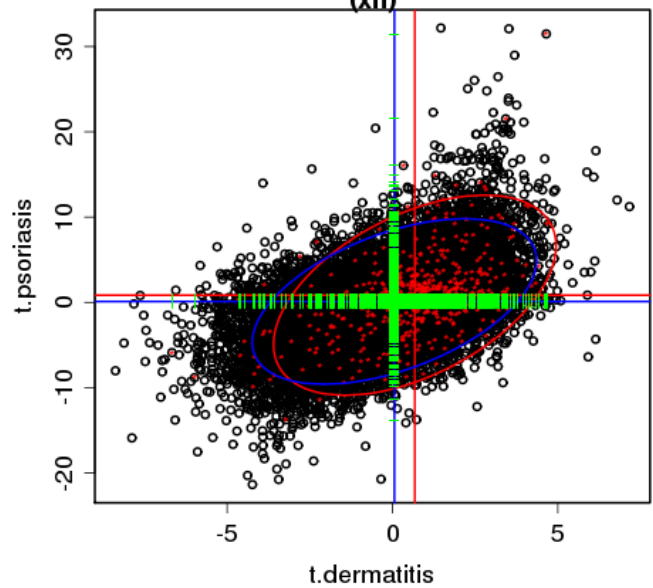
GO:0050878
regulation of body fluid levels (xh)



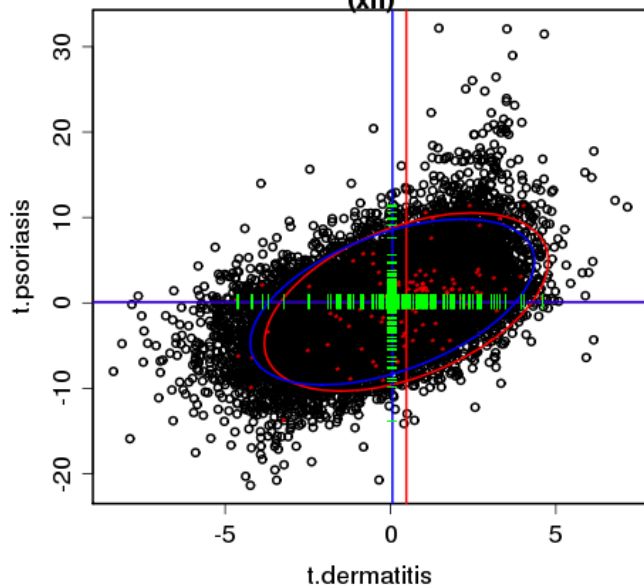
GO:0007599
hemostasis
(xh)



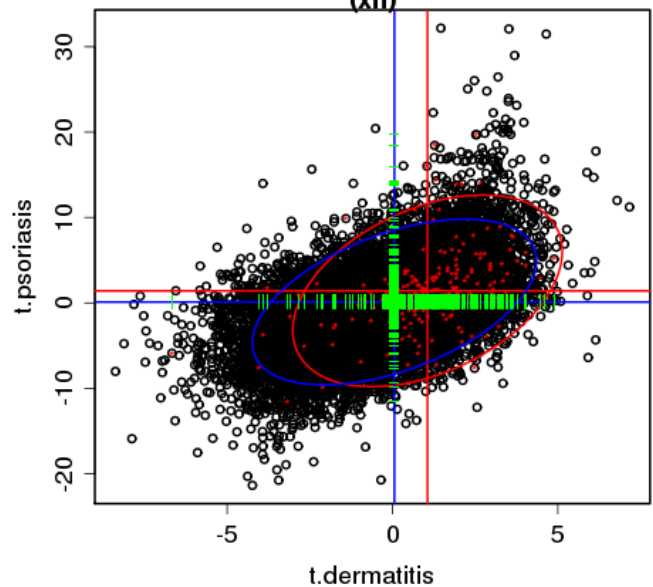
GO:0009611
response to wounding
(xh)



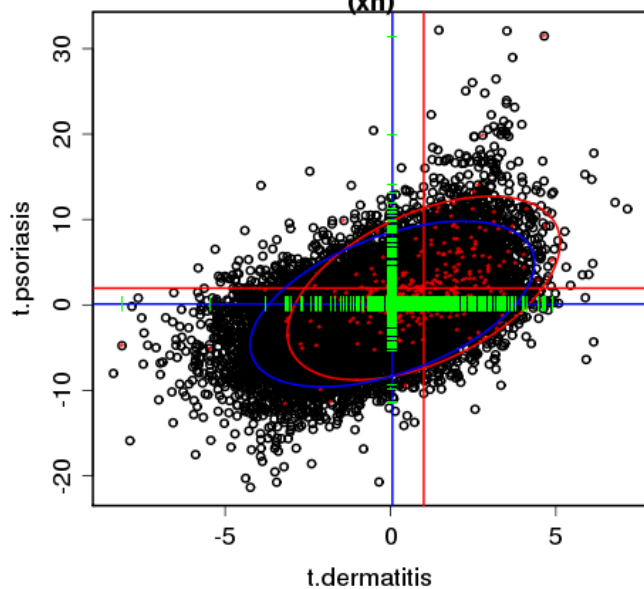
GO:0050817
coagulation
(xh)



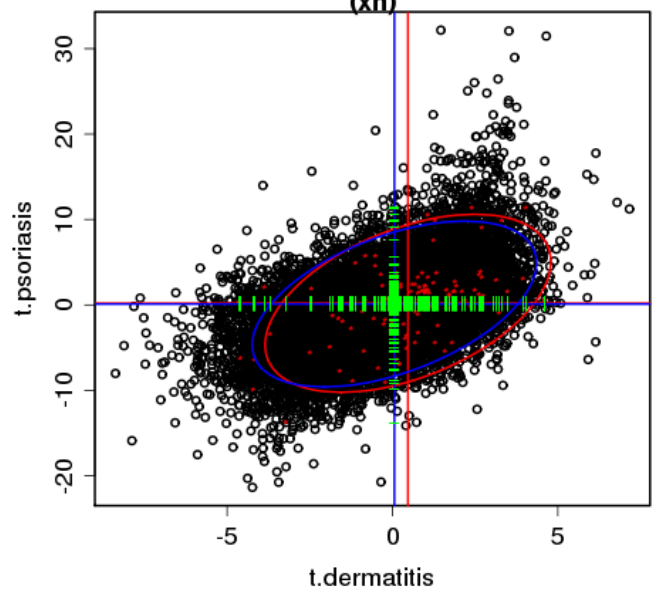
GO:0006959
humoral immune response
(xh)



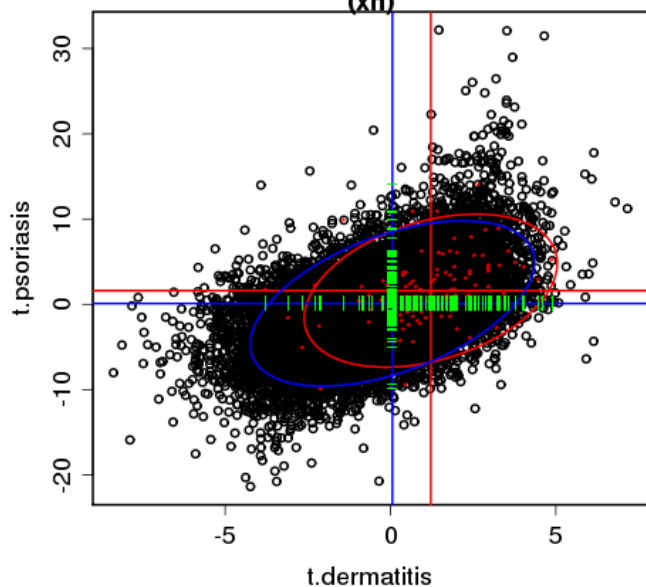
GO:0051707
response to other organism
(xh)



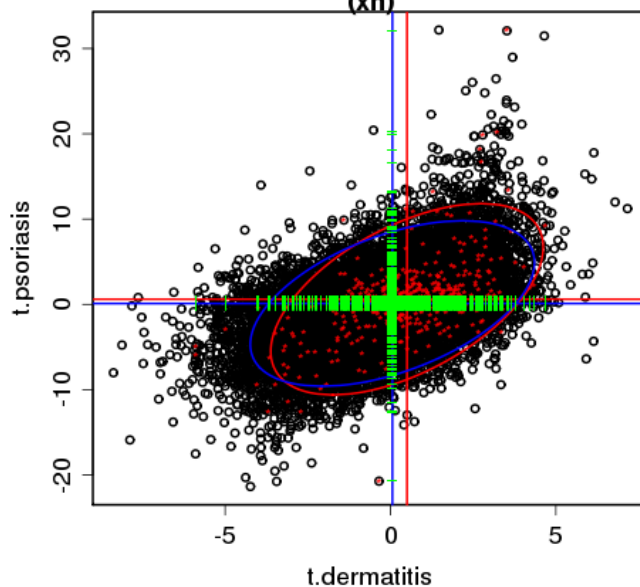
GO:0007596
blood coagulation
(xh)



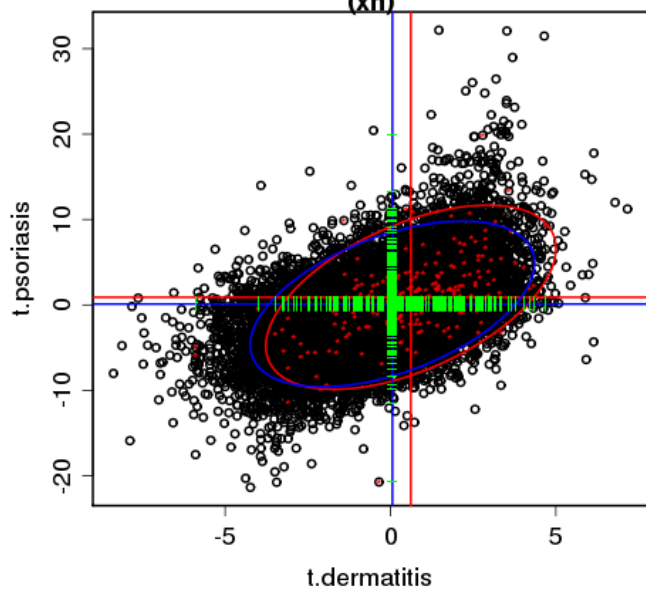
GO:0019730
antimicrobial humoral response
(xh)



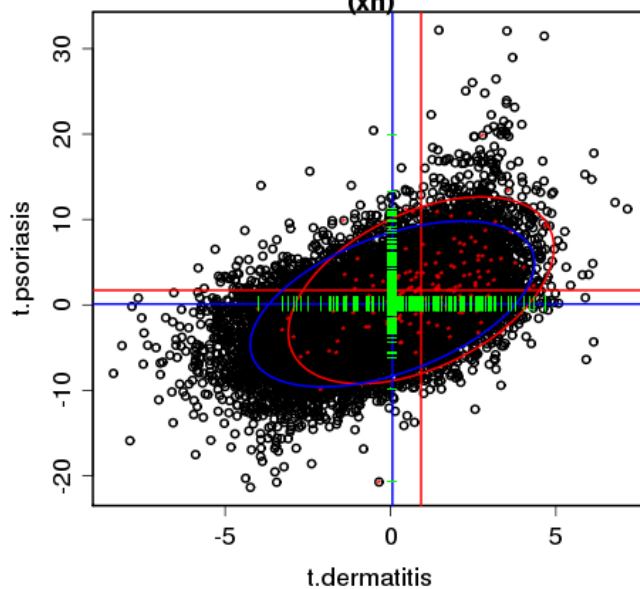
GO:0007610
behavior
(xh)



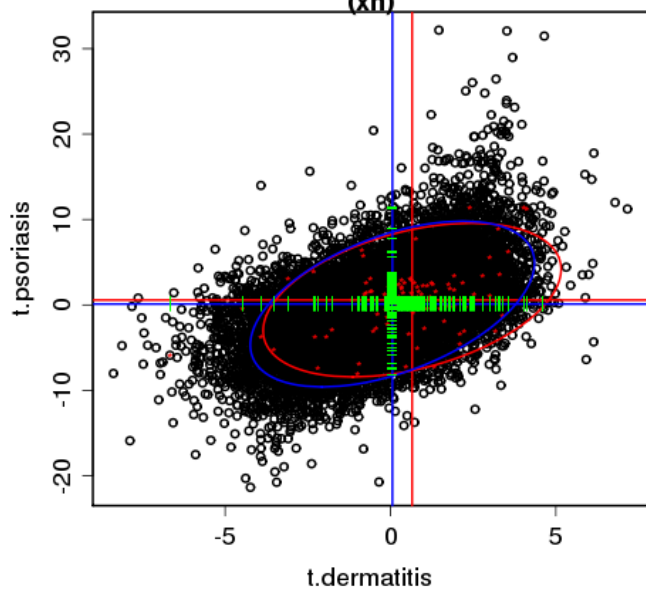
GO:0007626
locomotory behavior
(xh)



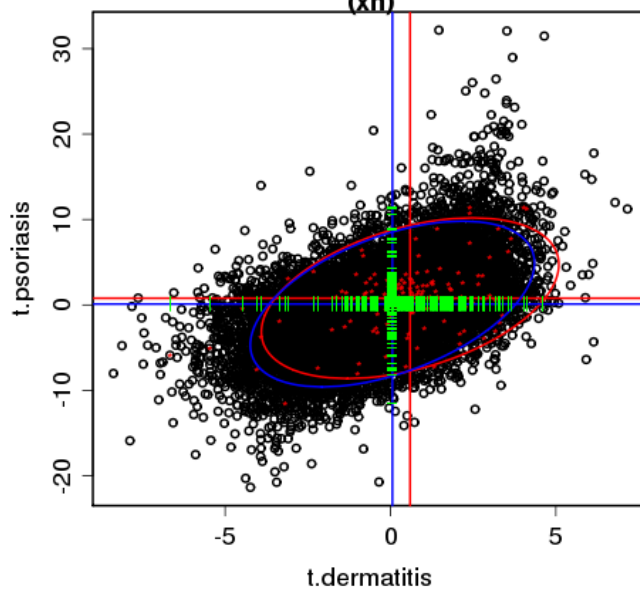
GO:0042330
taxis
(xh)



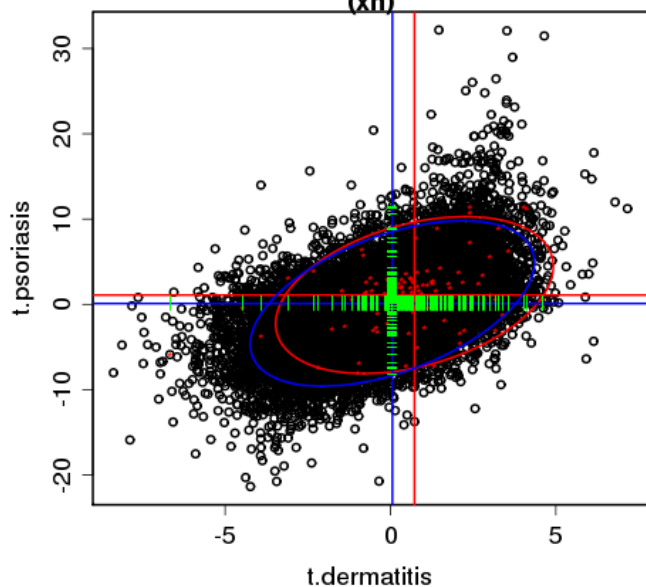
GO:0002250
adaptive immune response
(xh)



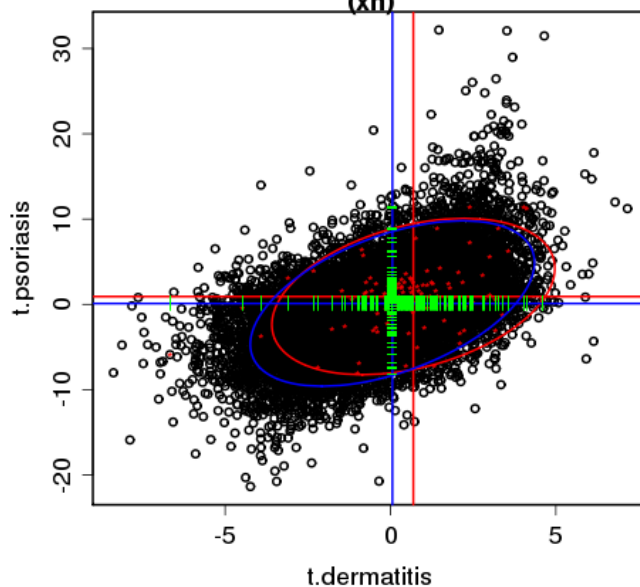
GO:0002252
immune effector process
(xh)



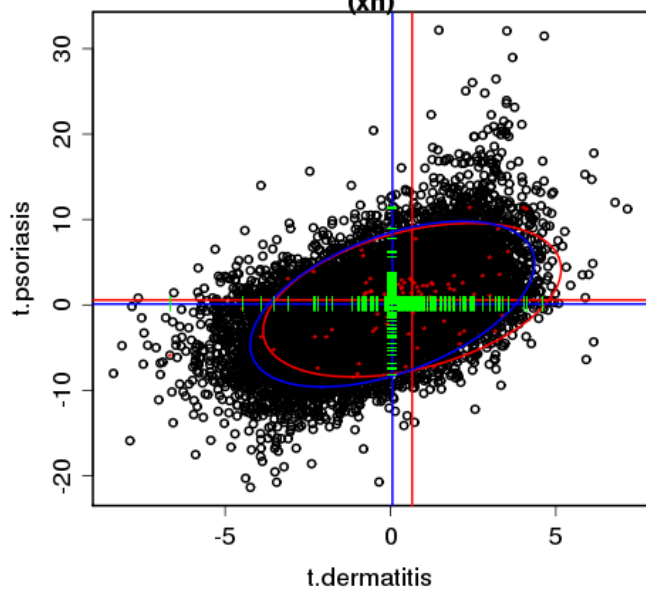
GO:0002443
leukocyte mediated immunity
(xh)



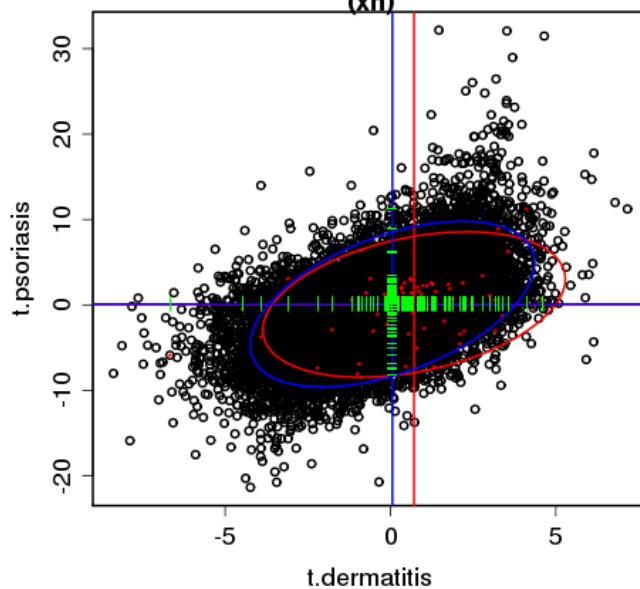
GO:0002449
lymphocyte mediated immunity
(xh)



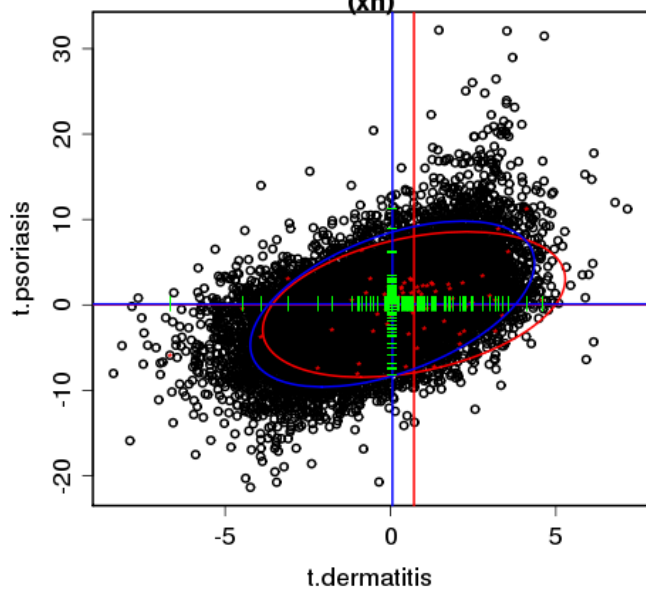
GO:0002460
n somatic recombination of immune receptors built from
(xh)



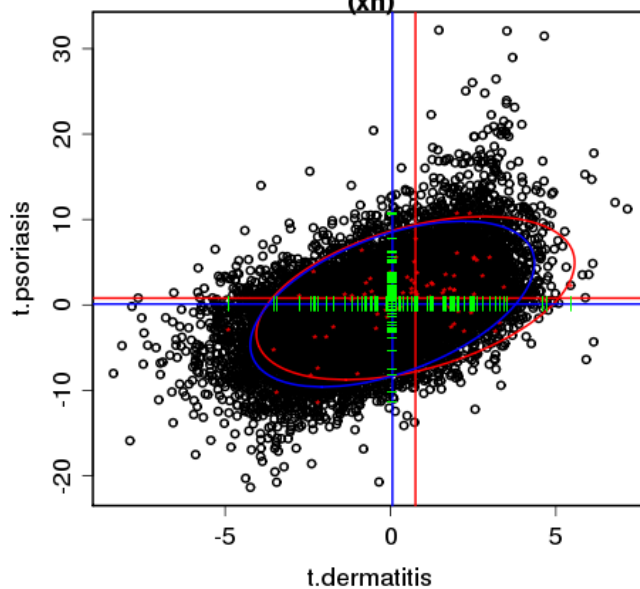
GO:0016064
immunoglobulin mediated immune response
(xh)



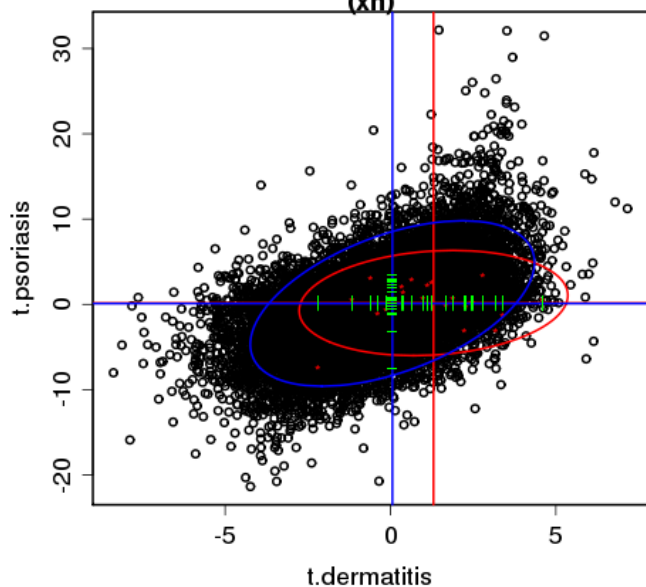
GO:0019724
B cell mediated immunity
(xh)



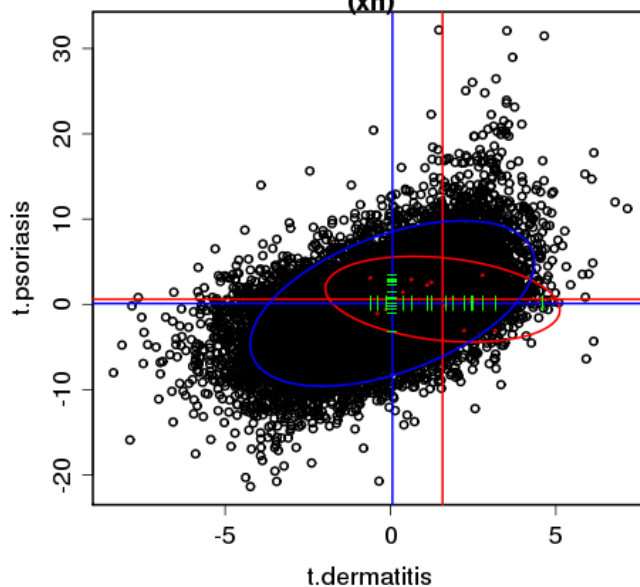
GO:0002696
positive regulation of leukocyte activation
(xh)



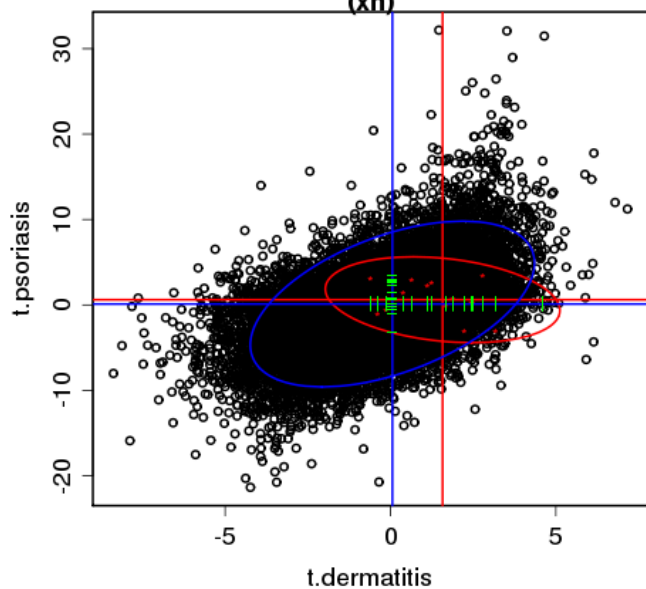
GO:0045191
regulation of isotype switching
(xh)



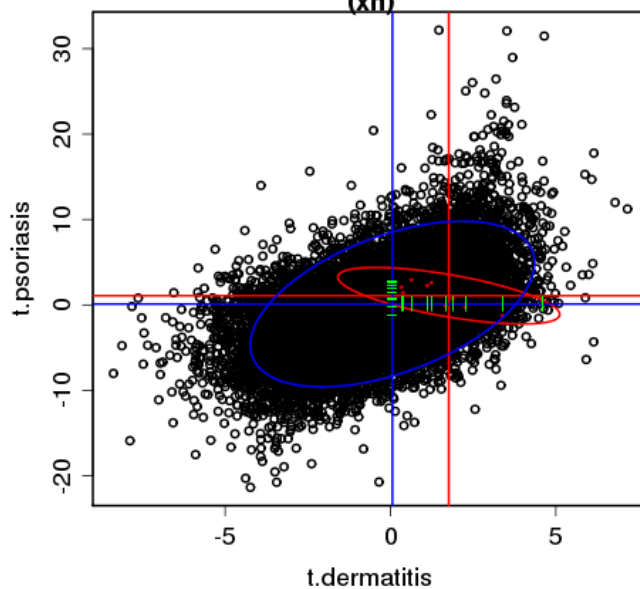
GO:0045830
positive regulation of isotype switching
(xh)



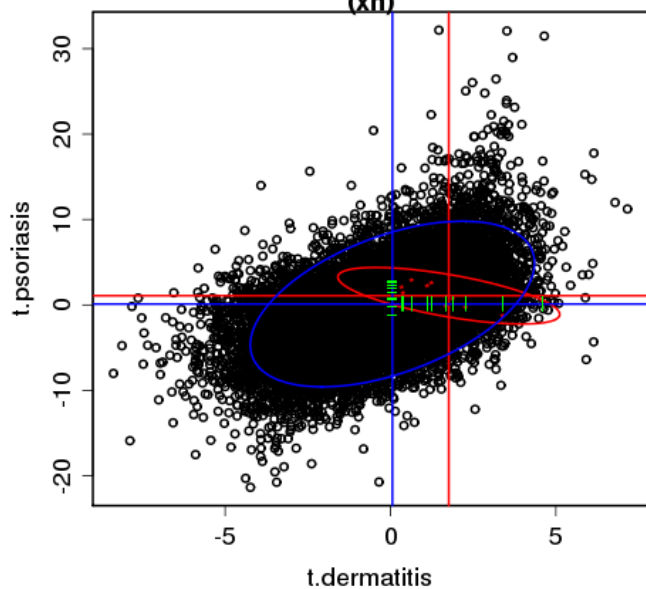
GO:0045911
positive regulation of DNA recombination
(xh)



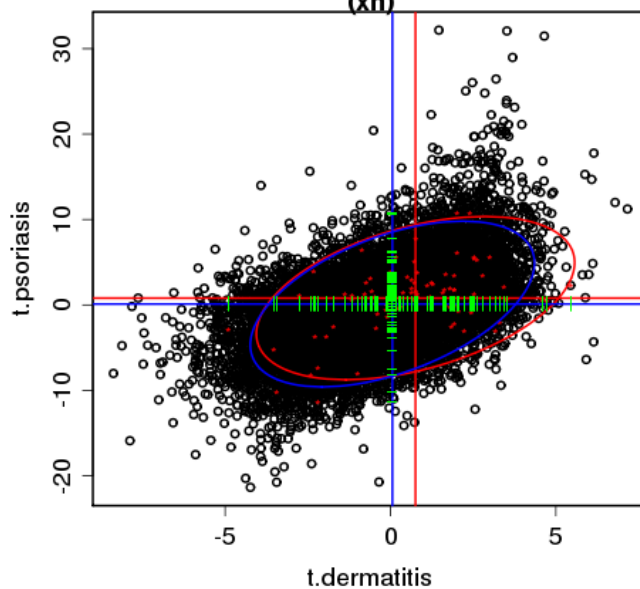
GO:0048291
isotype switching to IgG isotypes
(xh)

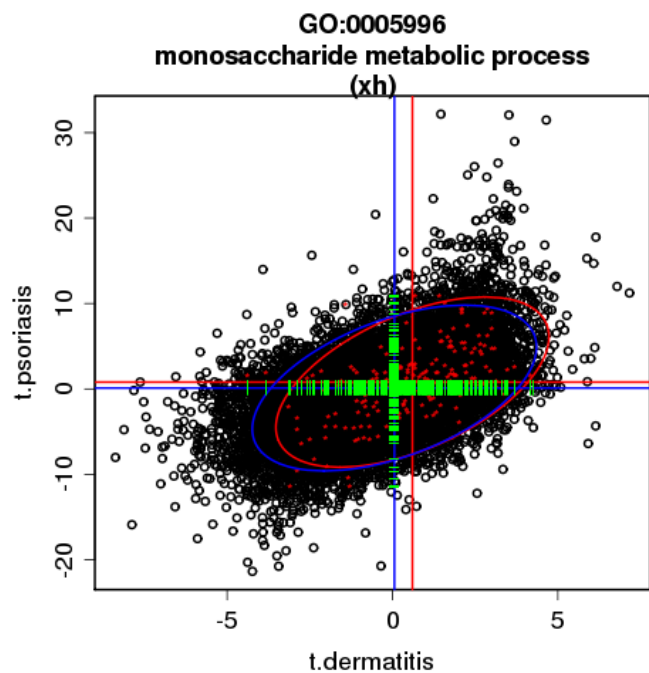
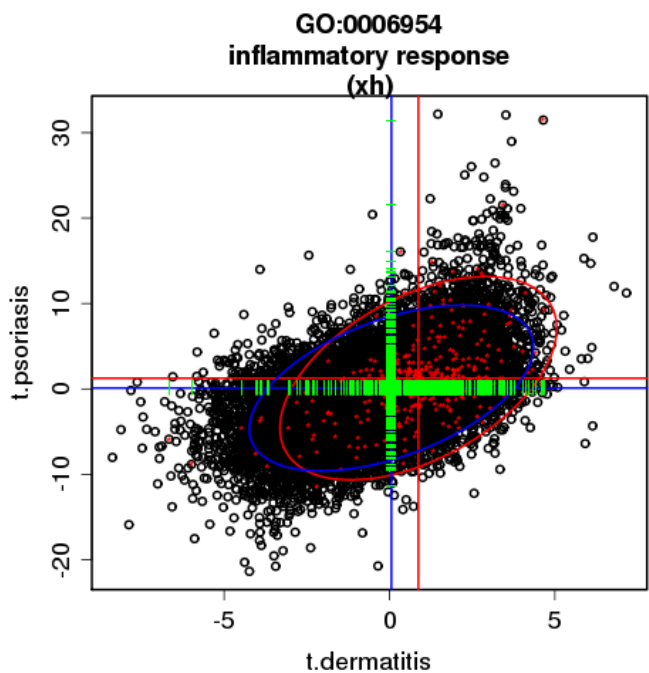
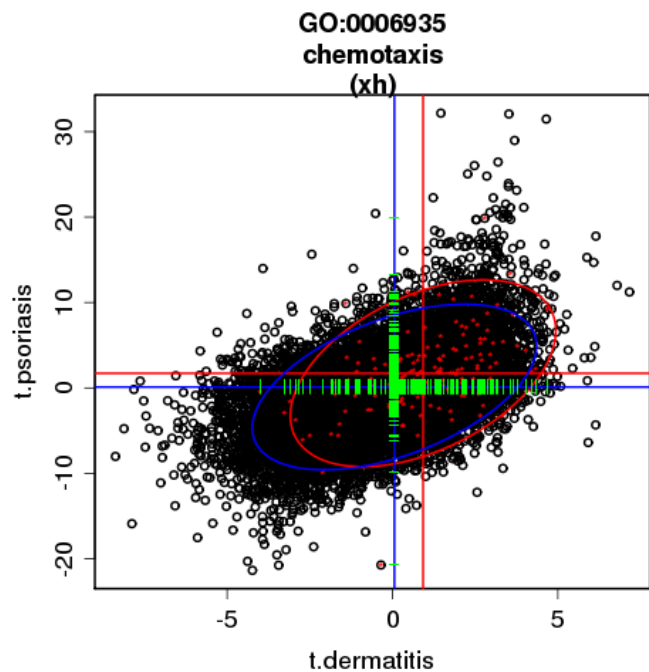
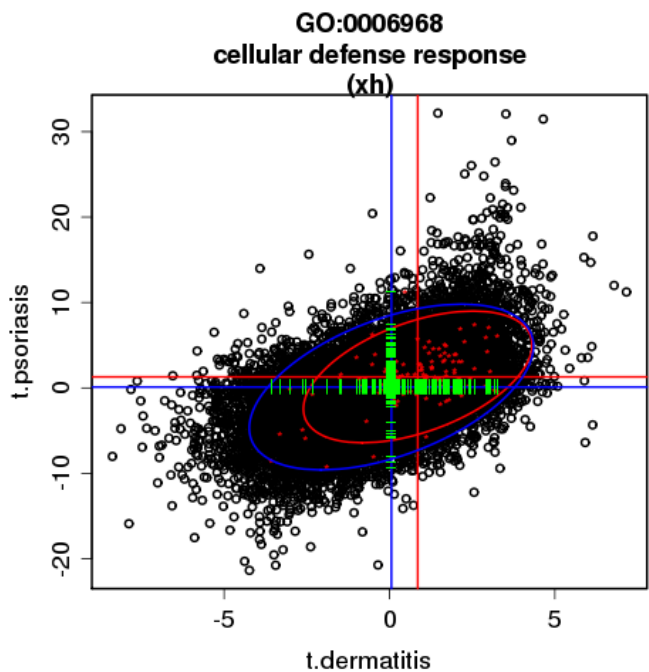
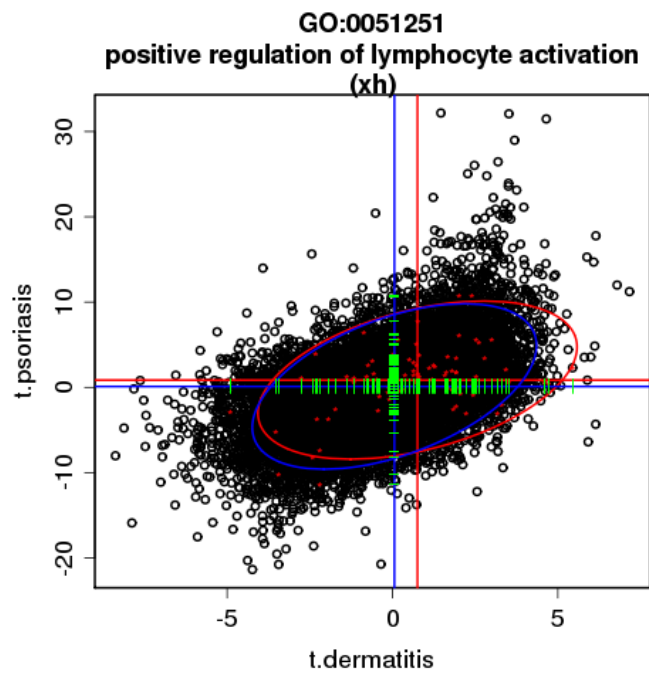
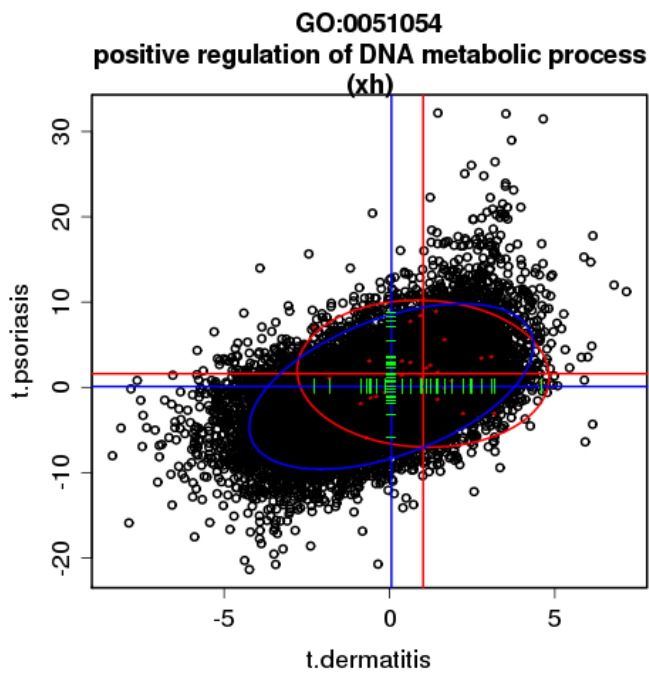


GO:0048302
regulation of isotype switching to IgG isotypes
(xh)

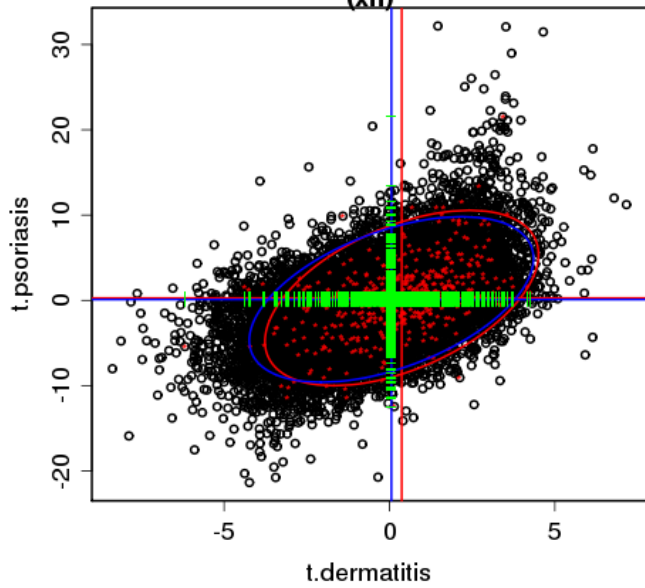


GO:0050867
positive regulation of cell activation
(xh)

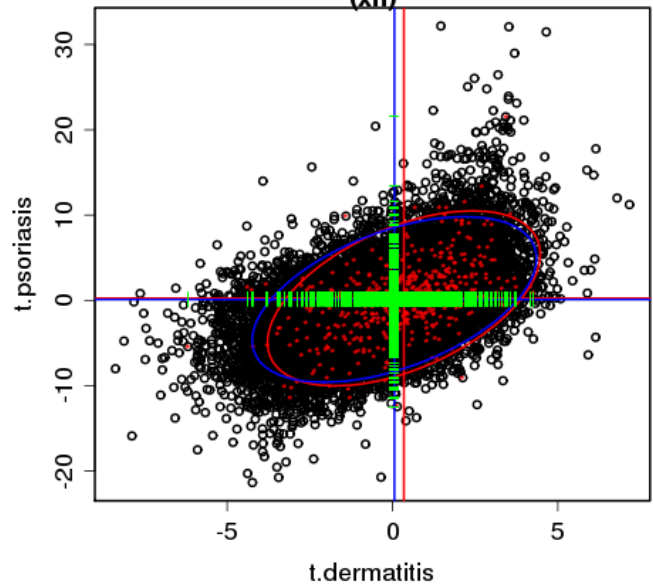




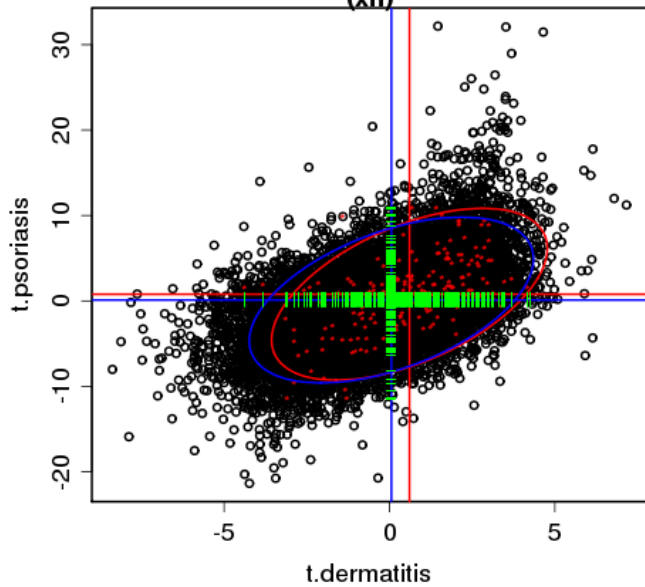
GO:0044262
cellular carbohydrate metabolic process
(xh)



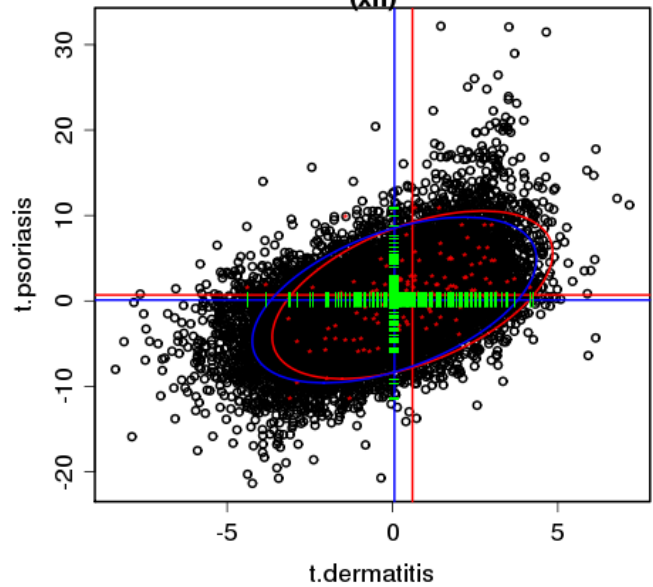
GO:0015980
energy derivation by oxidation of organic compounds
(xh)



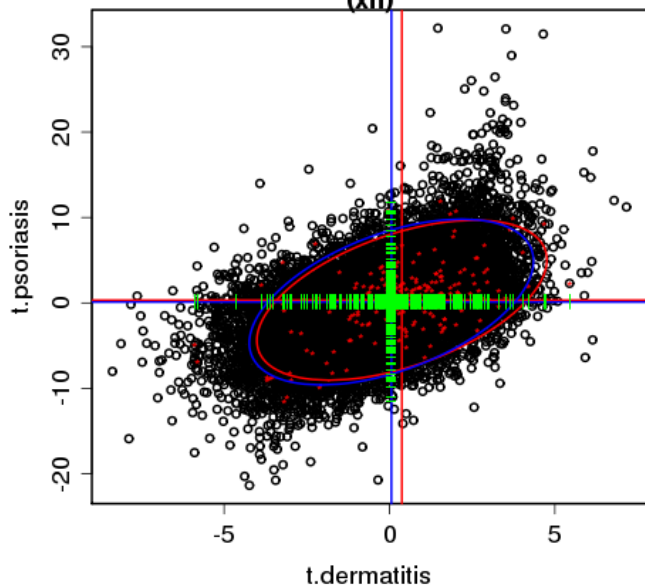
GO:0019318
hexose metabolic process
(xh)



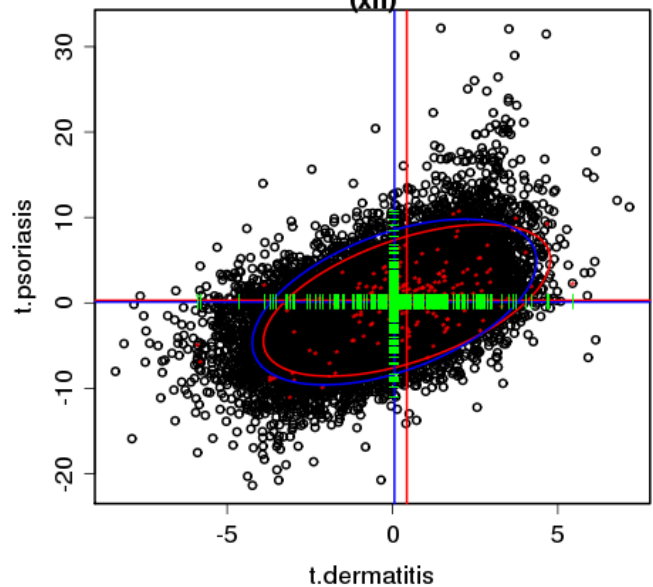
GO:0006006
glucose metabolic process
(xh)



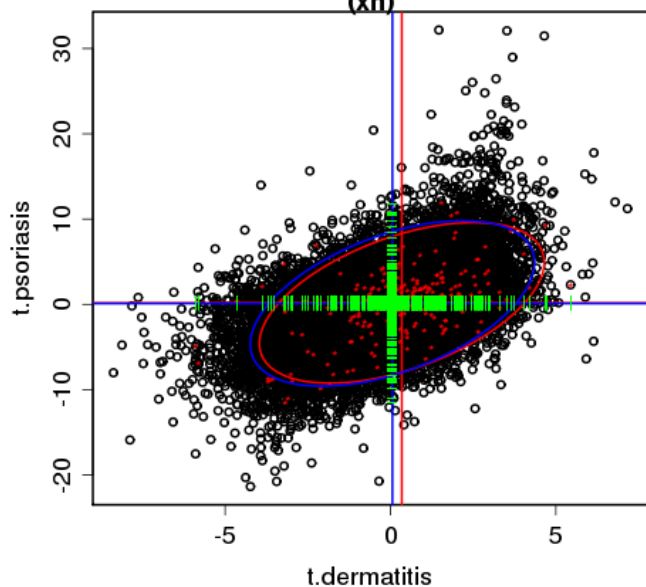
GO:0030003
cellular cation homeostasis
(xh)



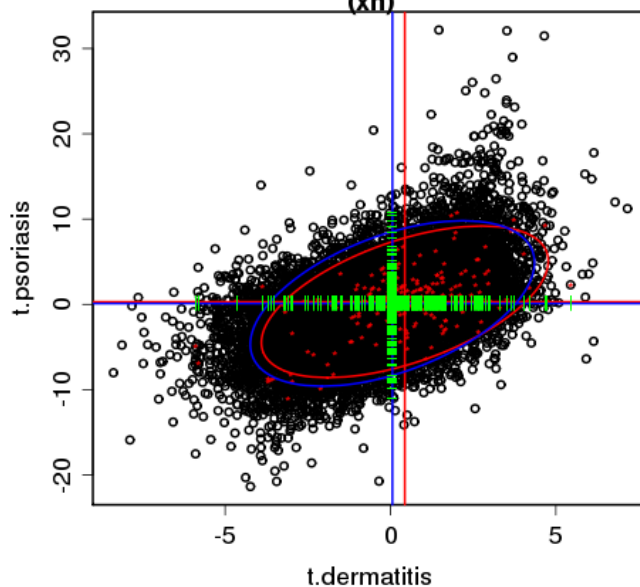
GO:0055065
metal ion homeostasis
(xh)



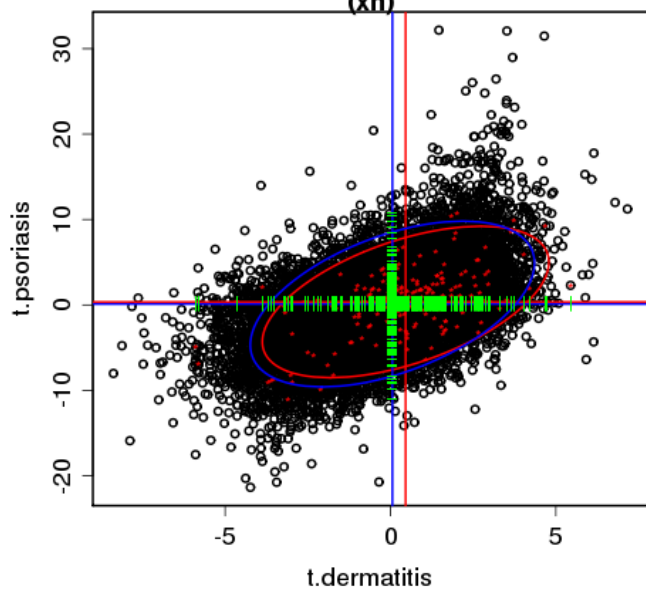
GO:0055080
cation homeostasis
(xh)



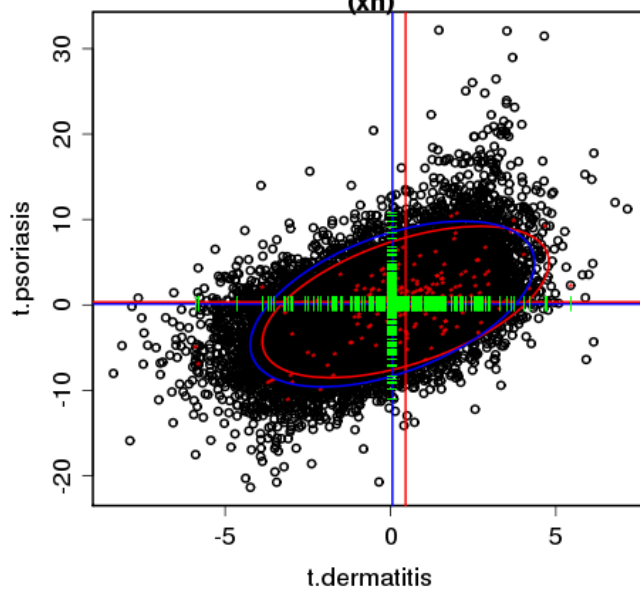
GO:0006875
cellular metal ion homeostasis
(xh)



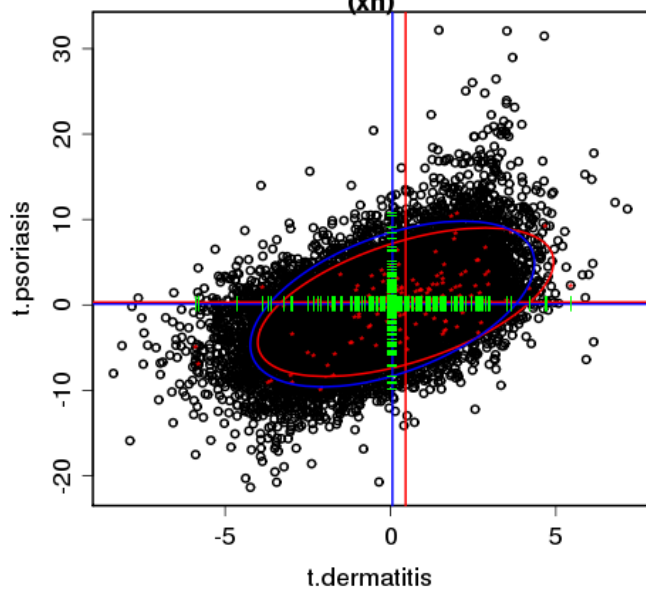
GO:0030005
cellular di-, tri-valent inorganic cation homeostasis
(xh)



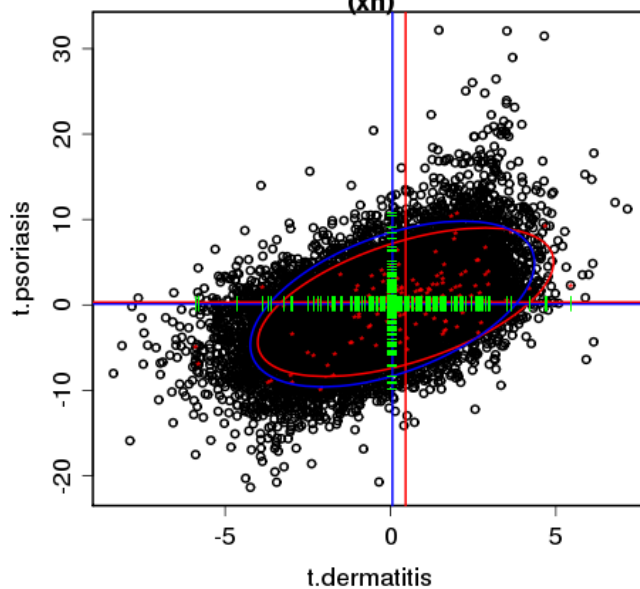
GO:0055066
di-, tri-valent inorganic cation homeostasis
(xh)



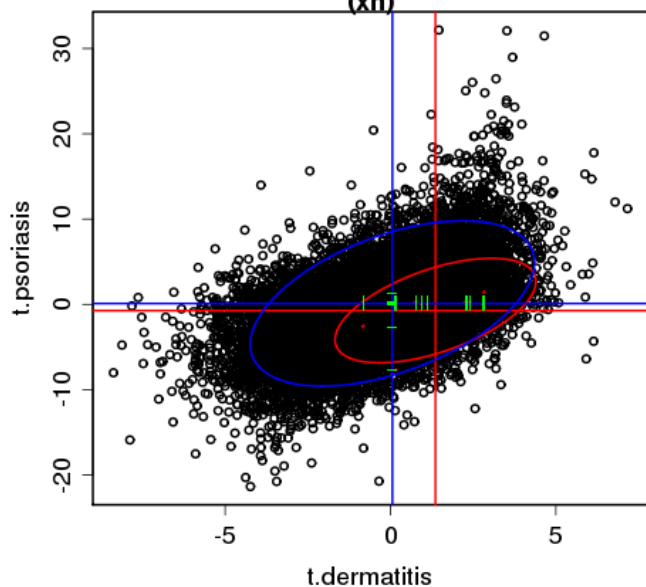
GO:0055074
calcium ion homeostasis
(xh)



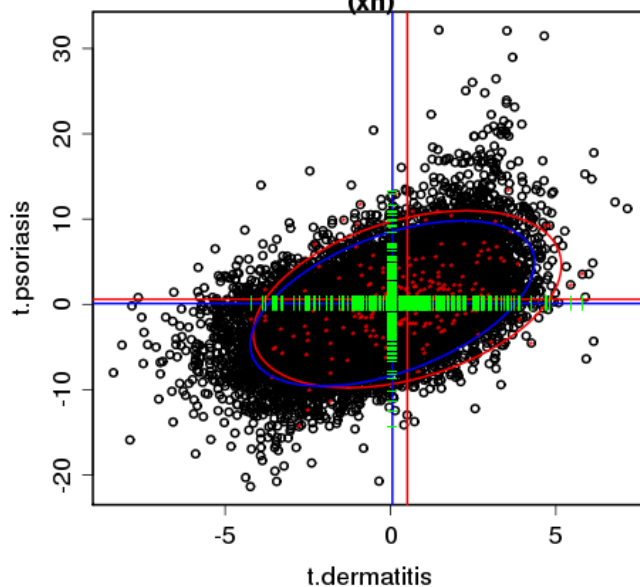
GO:0006874
cellular calcium ion homeostasis
(xh)



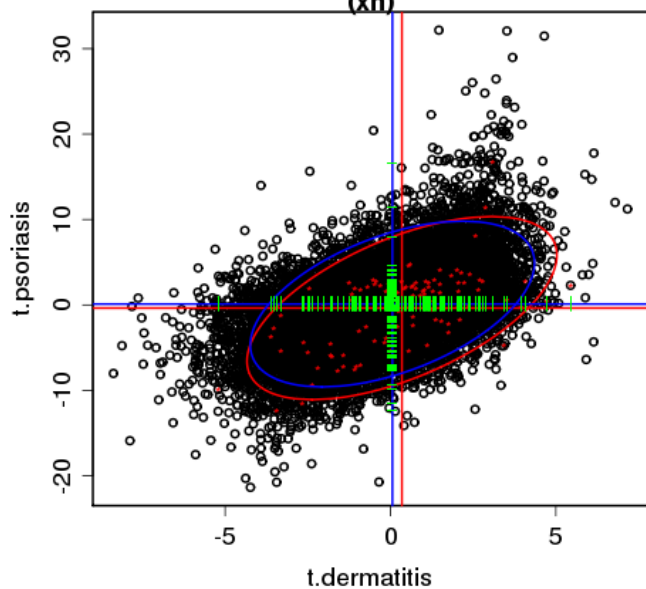
GO:0045214
sarcomere organization
(xh)



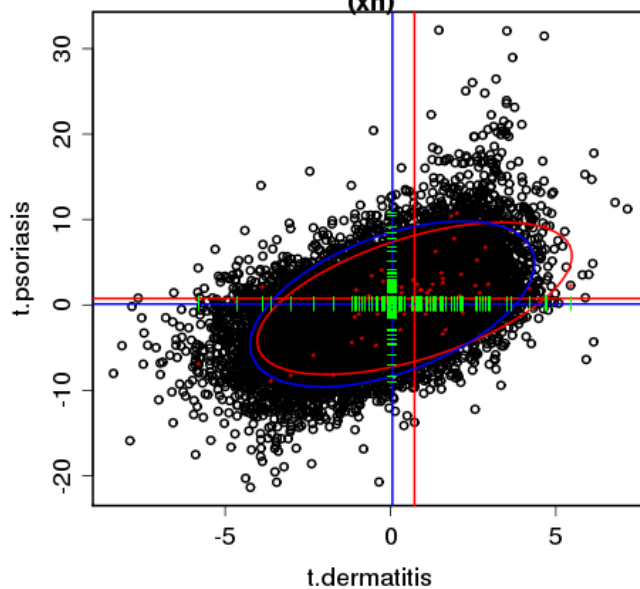
GO:0048646
anatomical structure formation
(xh)



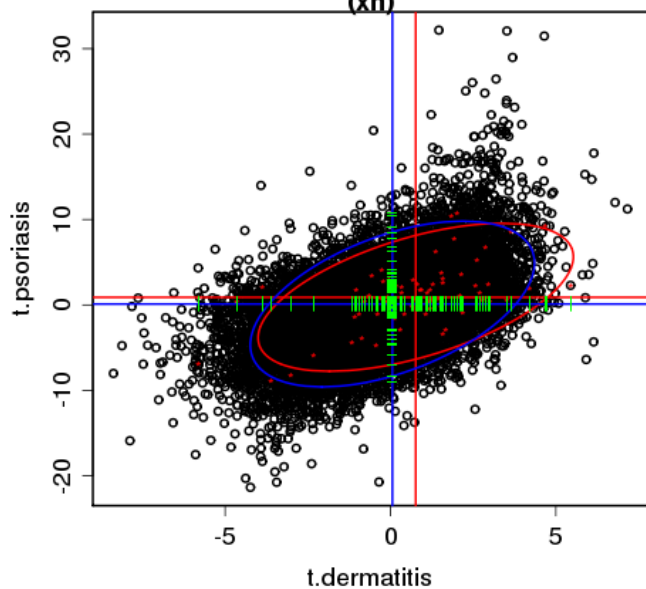
GO:0007160
cell-matrix adhesion
(xh)



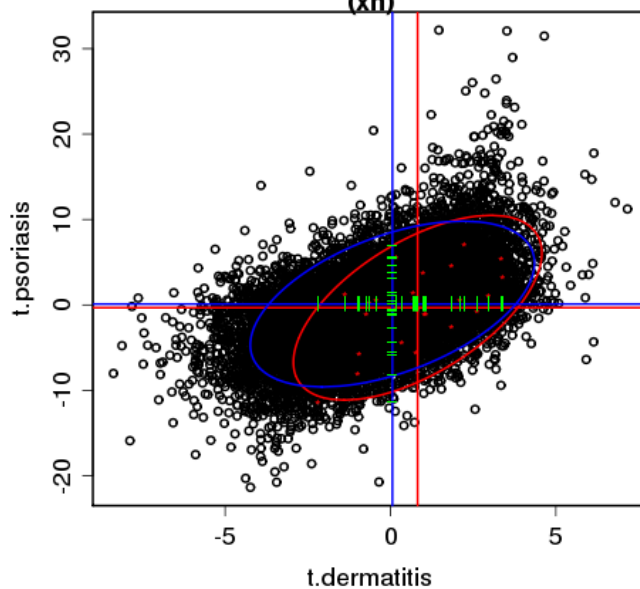
GO:0051480
cytosolic calcium ion homeostasis
(xh)



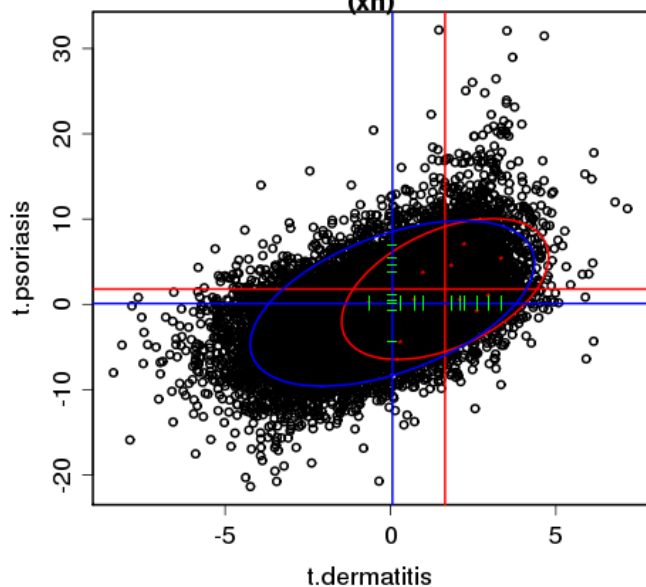
GO:0007204
elevation of cytosolic calcium ion concentration
(xh)



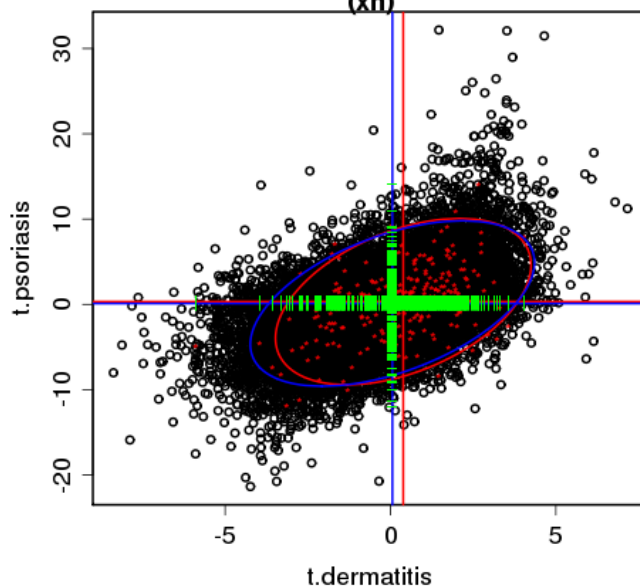
GO:0032103
positive regulation of response to external stimulus
(xh)



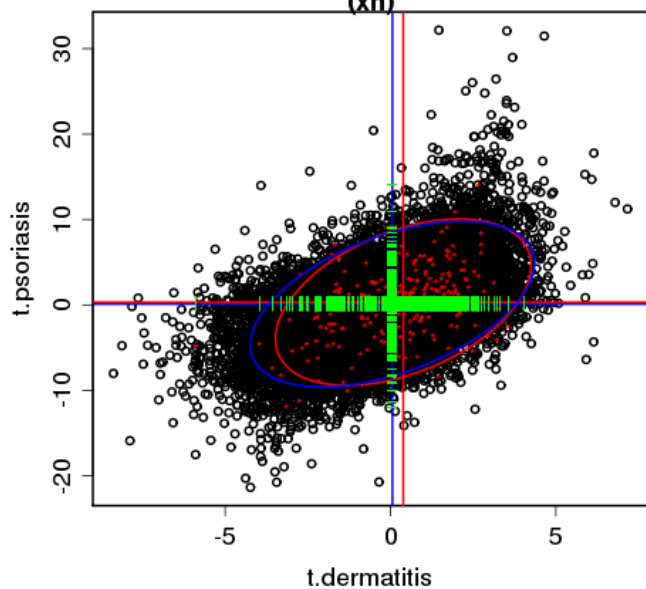
GO:0050920
regulation of chemotaxis
(xh)



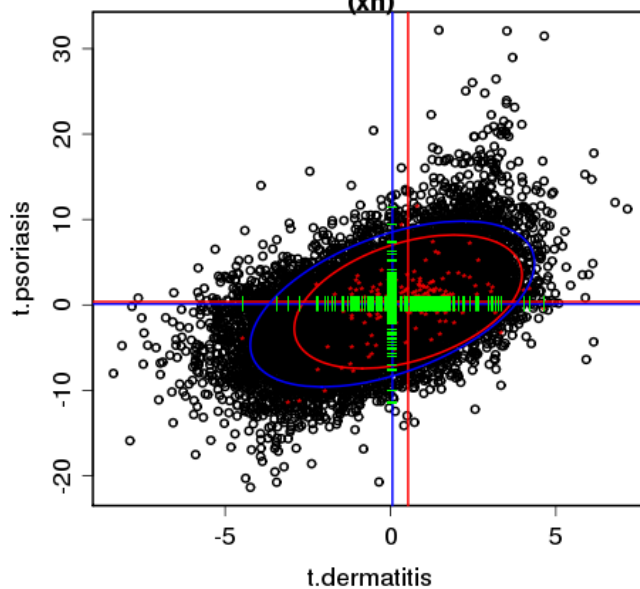
GO:0006897
endocytosis
(xh)



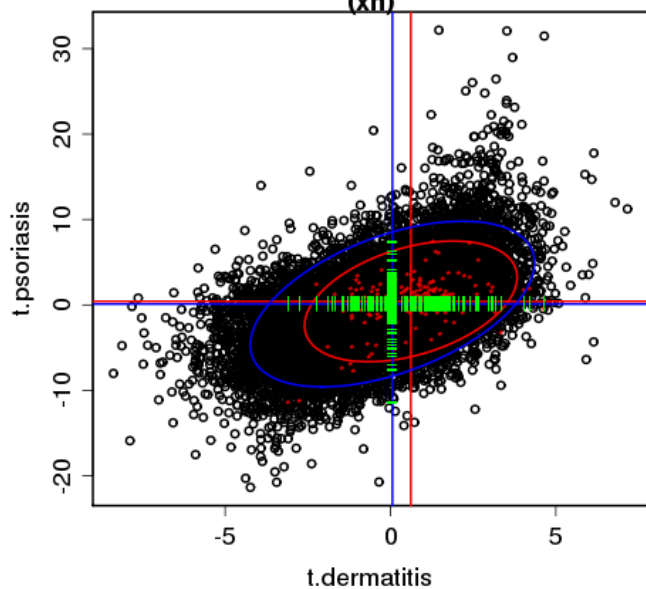
GO:0010324
membrane invagination
(xh)



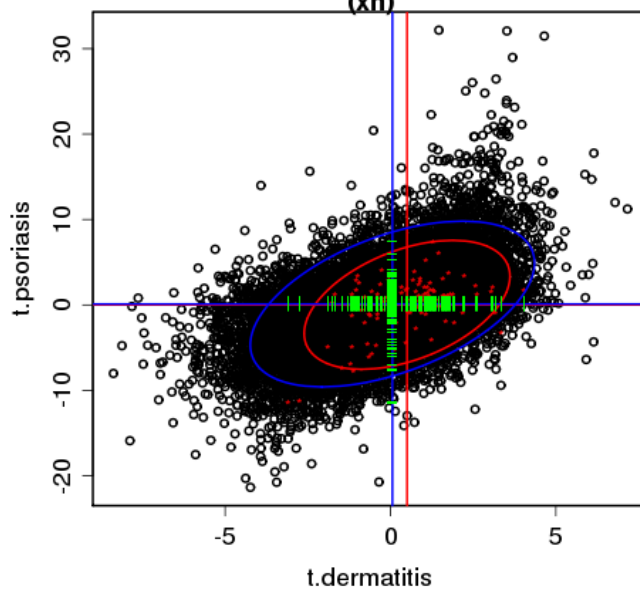
GO:0019935
cyclic-nucleotide-mediated signaling
(xh)



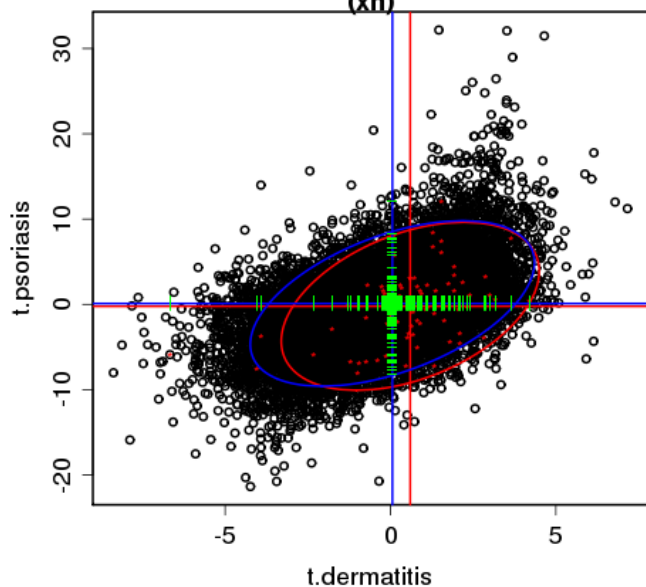
GO:0007187
protein signaling, coupled to cyclic nucleotide second messenger
(xh)



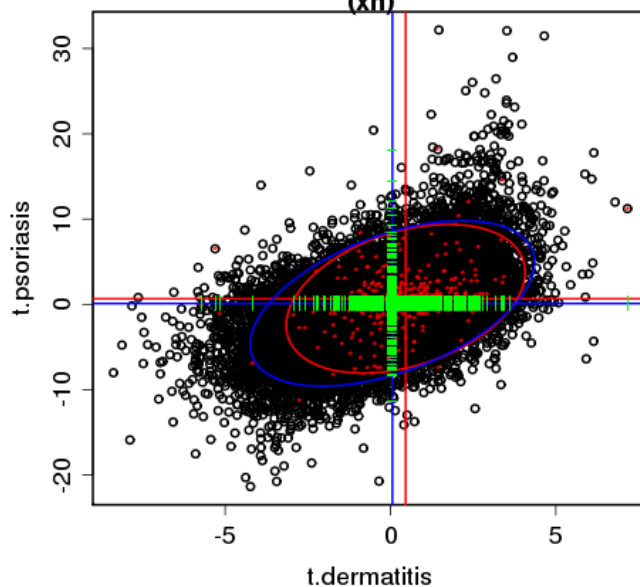
GO:0007188
protein signaling, coupled to cAMP nucleotide second messenger
(xh)



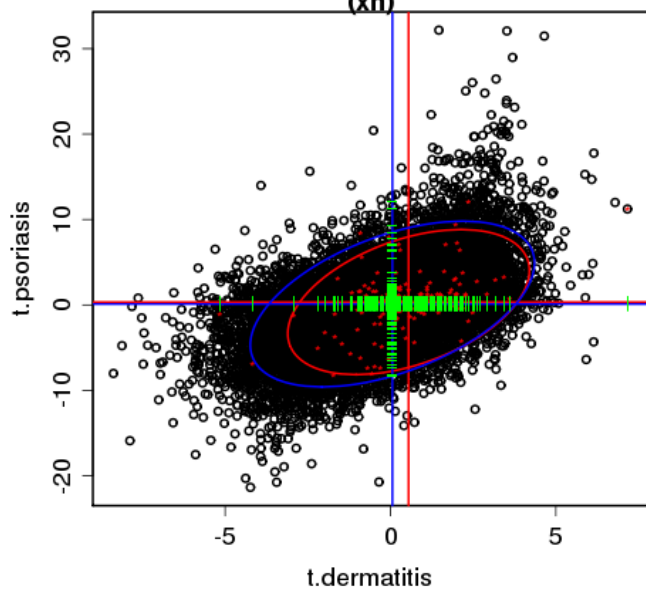
GO:0002526
acute inflammatory response
(xh)



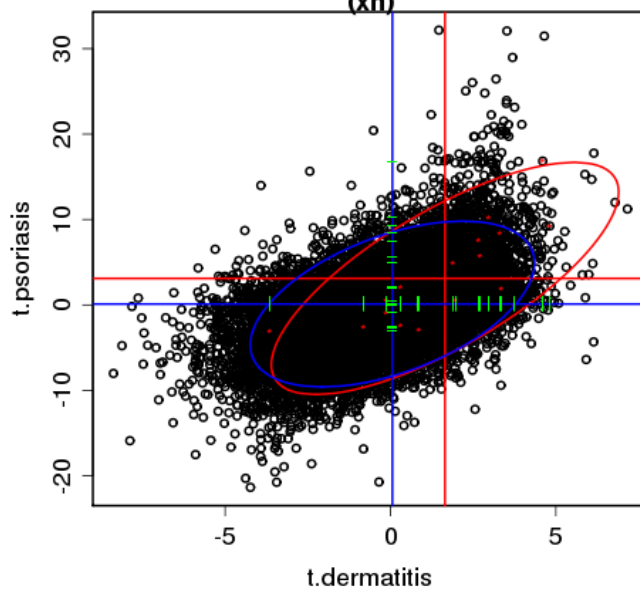
GO:0015672
monovalent inorganic cation transport
(xh)



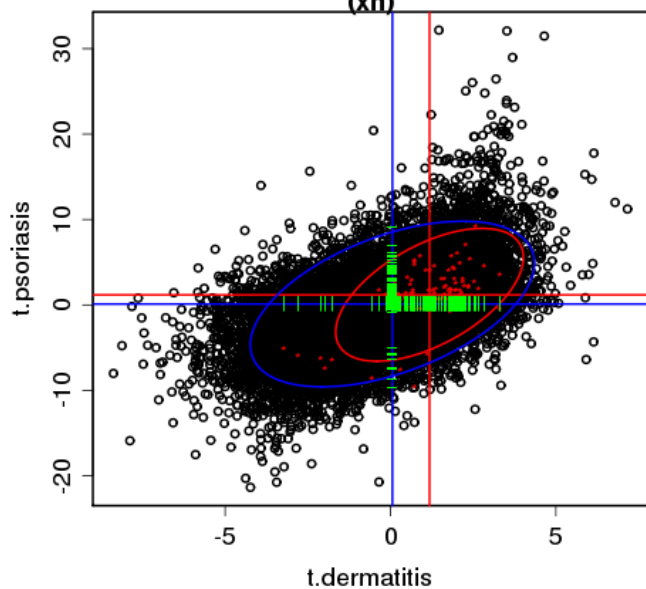
GO:0006813
potassium ion transport
(xh)



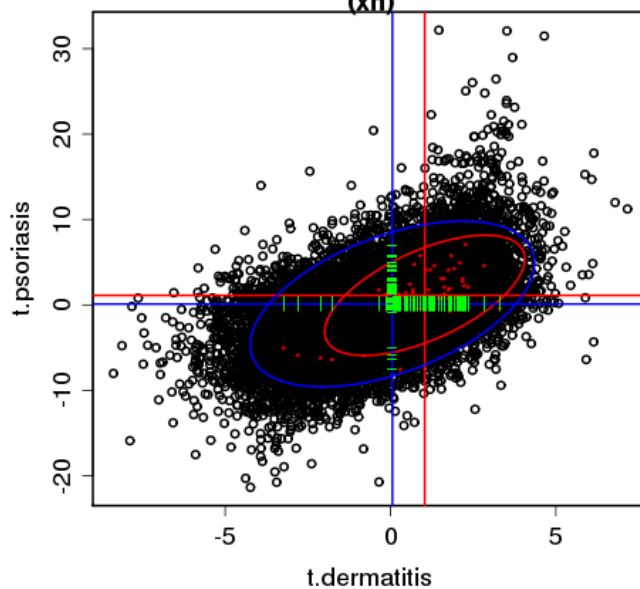
GO:0051346
negative regulation of hydrolase activity
(xh)



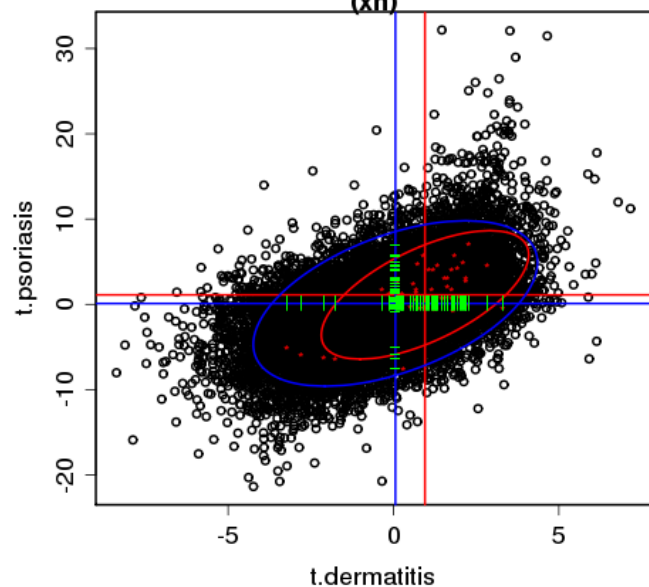
GO:0019882
antigen processing and presentation
(xh)



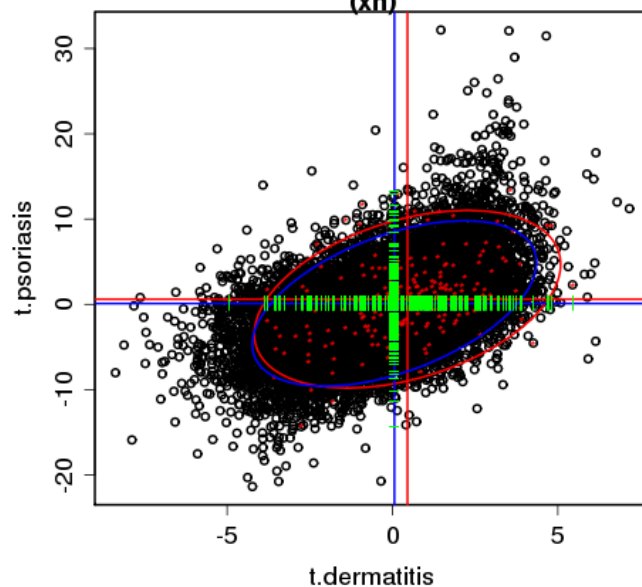
GO:0048002
antigen processing and presentation of peptide antigen
(xh)



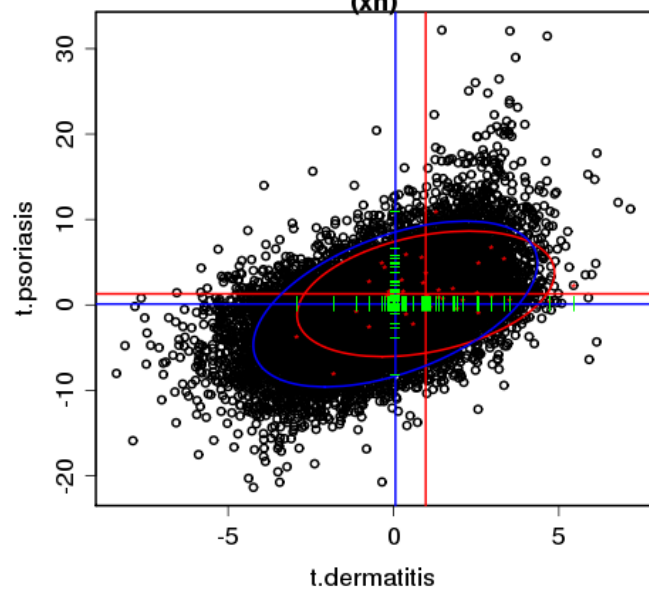
GO:0002474
in processing and presentation of peptide antigen via MHC class II (xh)



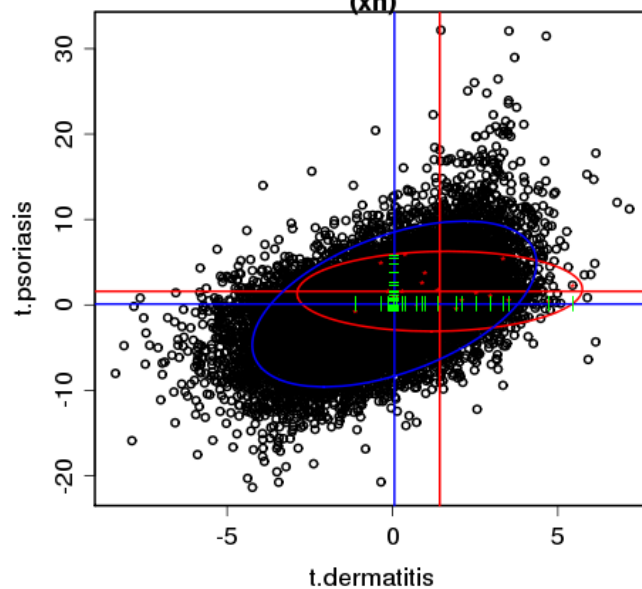
GO:0048514
blood vessel morphogenesis (xh)



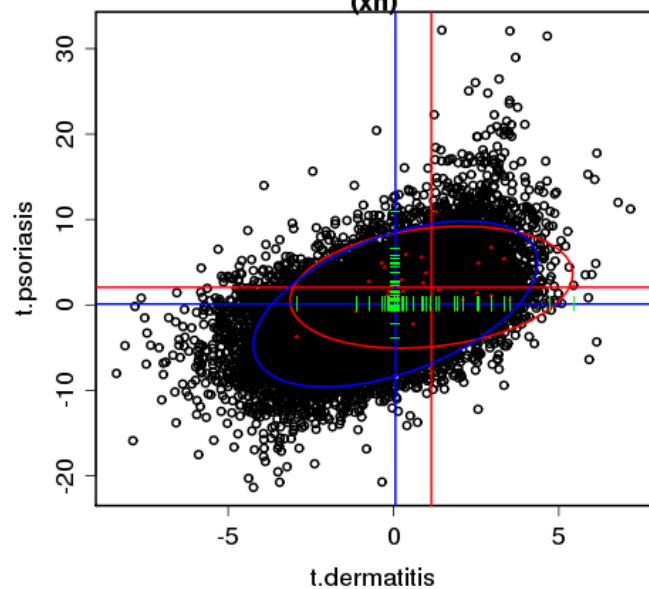
GO:0001654
eye development (xh)



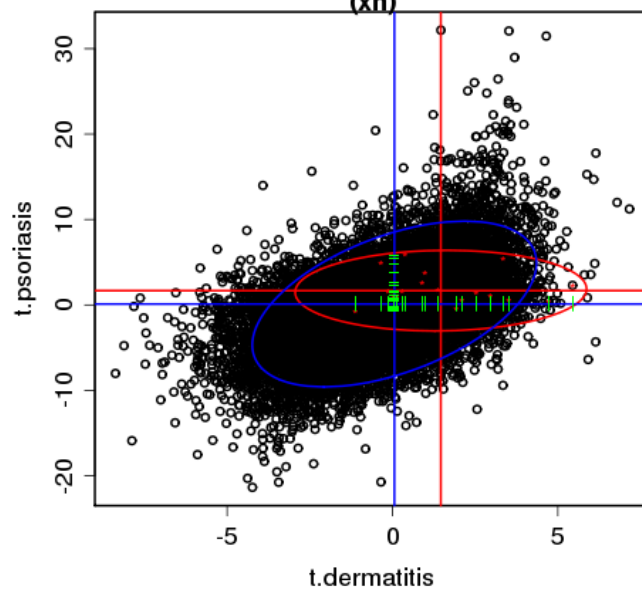
GO:0046530
photoreceptor cell differentiation (xh)



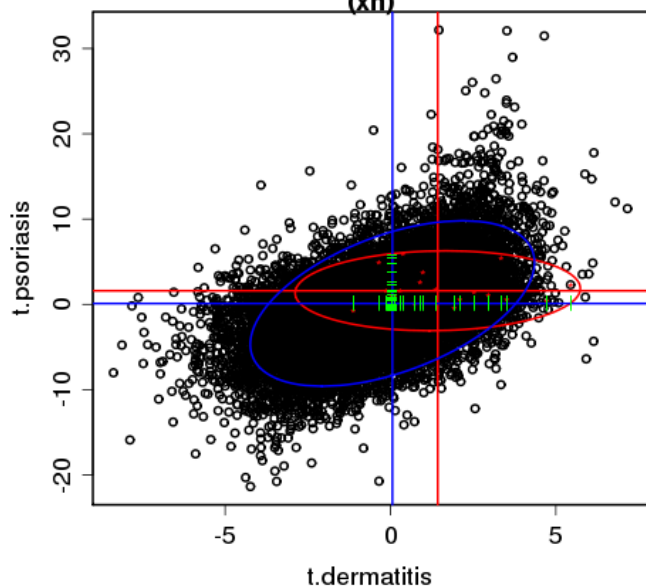
GO:0048592
eye morphogenesis (xh)



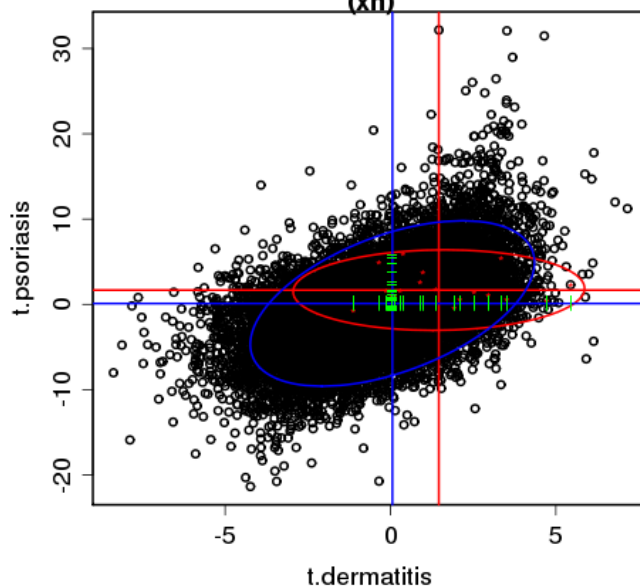
GO:0001754
eye photoreceptor cell differentiation (xh)



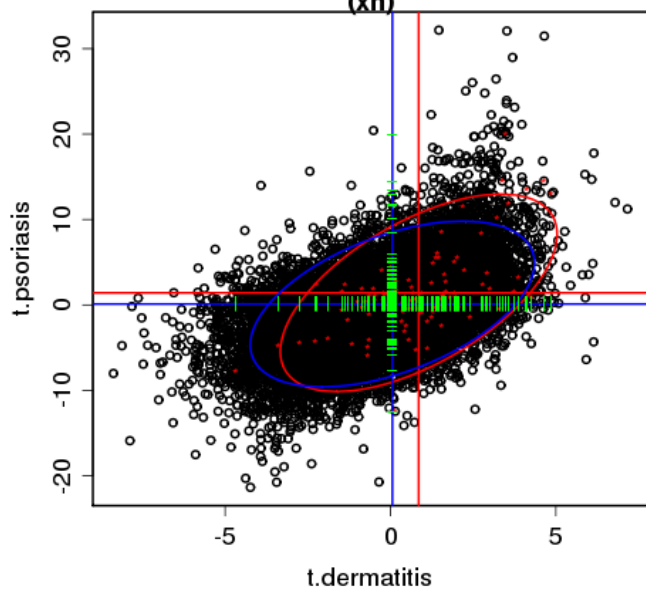
GO:0042461
photoreceptor cell development
(xh)



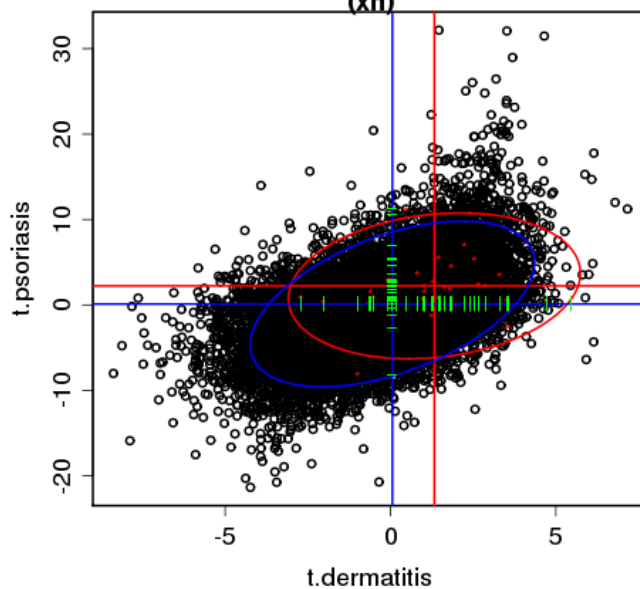
GO:0042462
eye photoreceptor cell development
(xh)



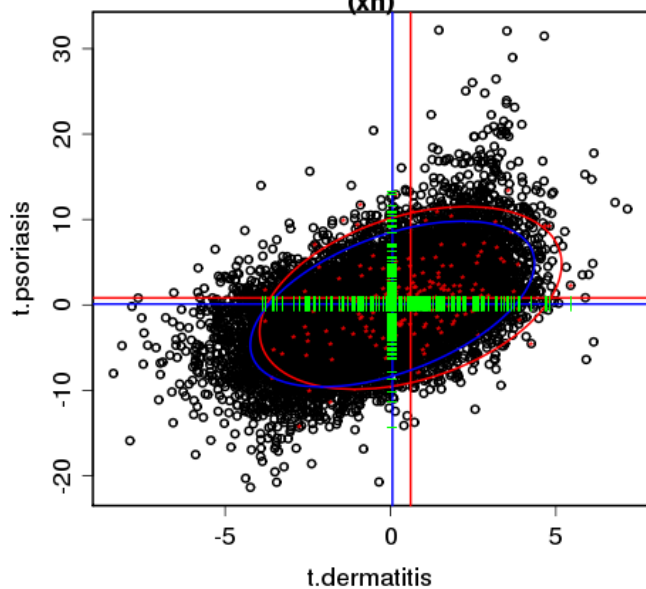
GO:0007586
digestion
(xh)



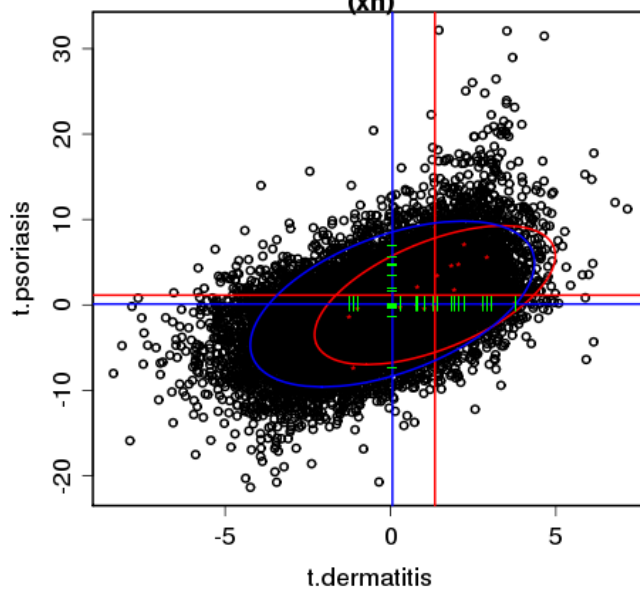
GO:0002274
myeloid leukocyte activation
(xh)



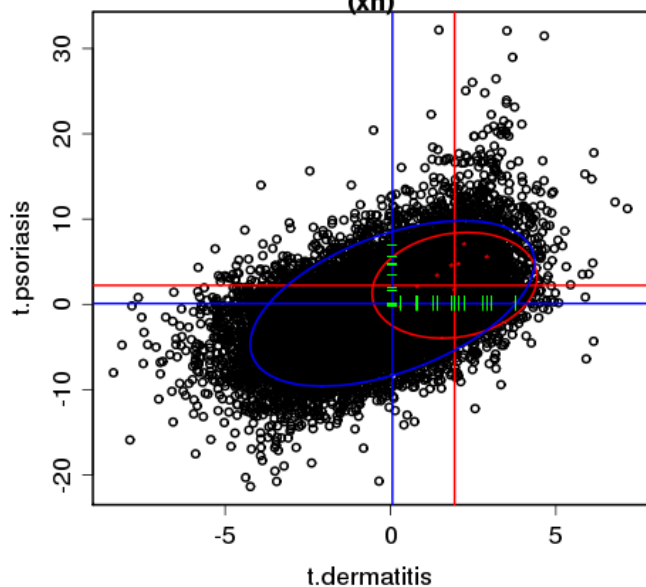
GO:0001525
angiogenesis
(xh)



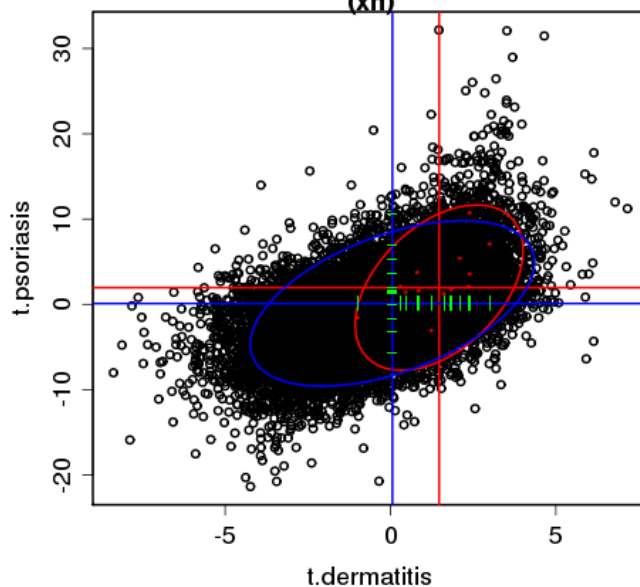
GO:0050792
regulation of viral reproduction
(xh)



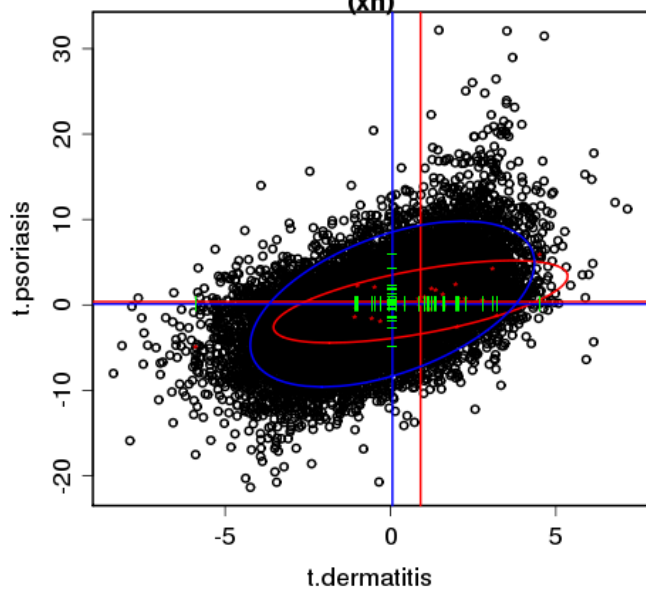
GO:0045069
regulation of viral genome replication
(xh)



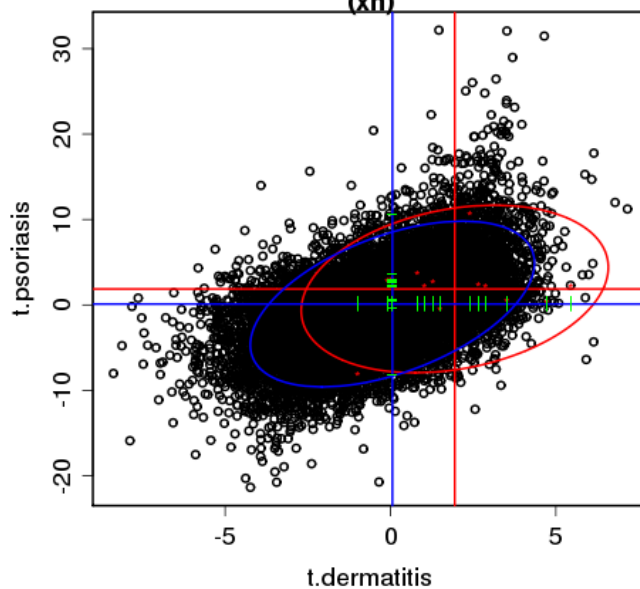
GO:0007159
leukocyte adhesion
(xh)



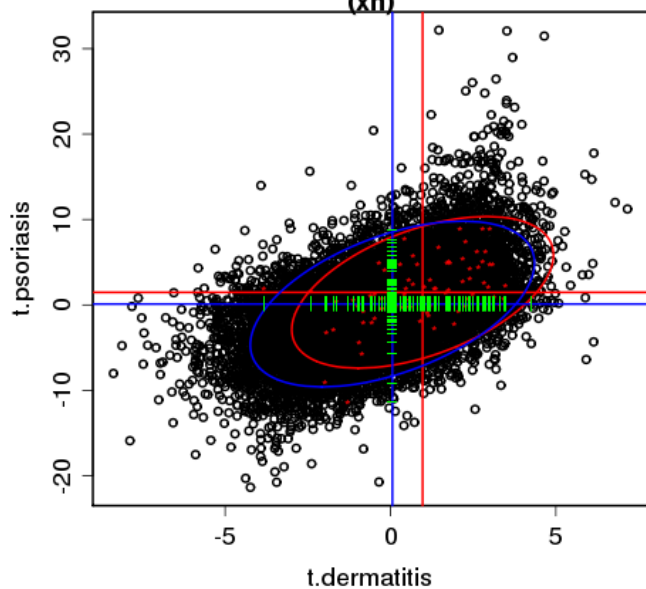
GO:0007416
synaptogenesis
(xh)



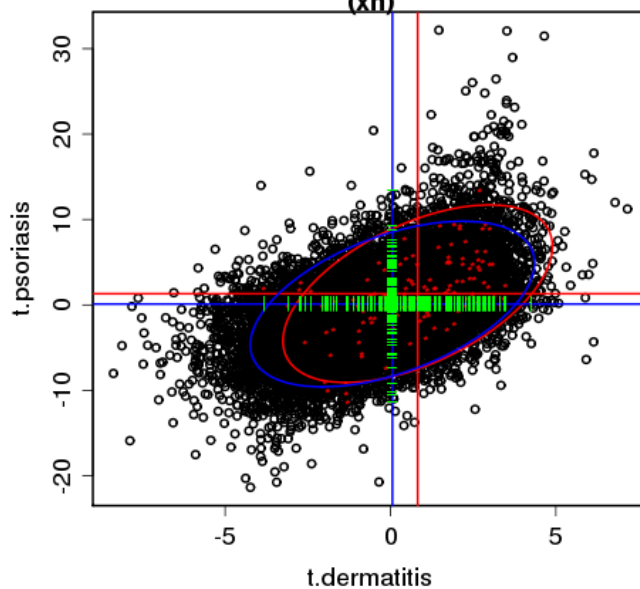
GO:0045576
mast cell activation
(xh)

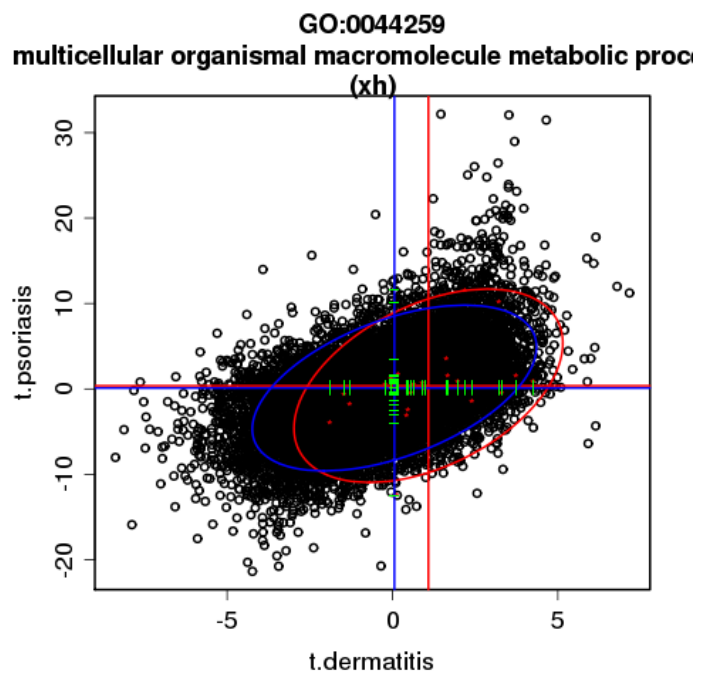
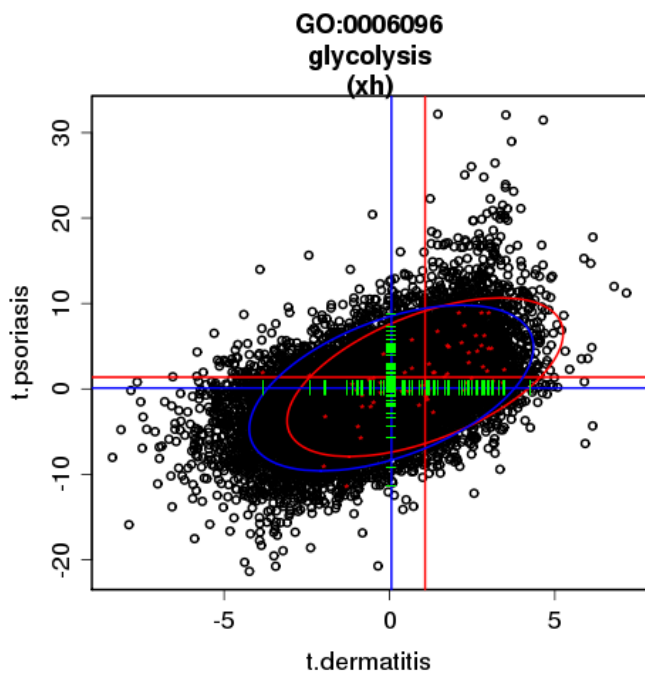
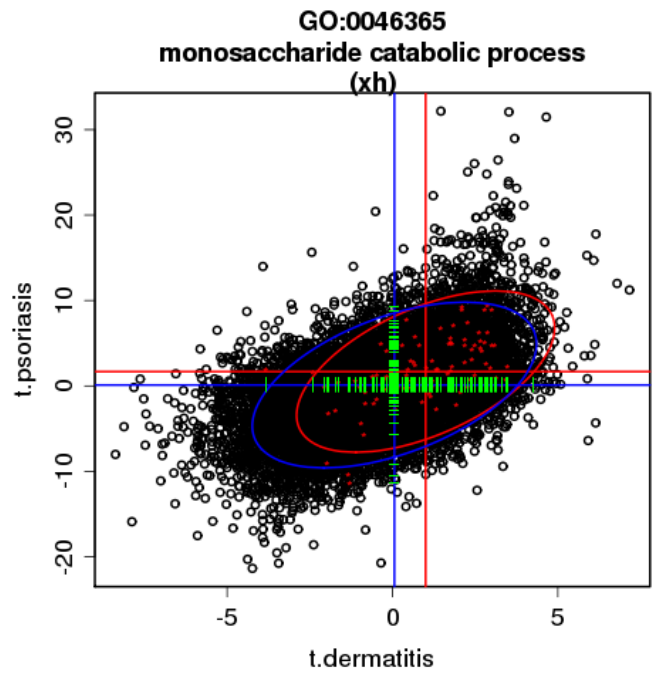
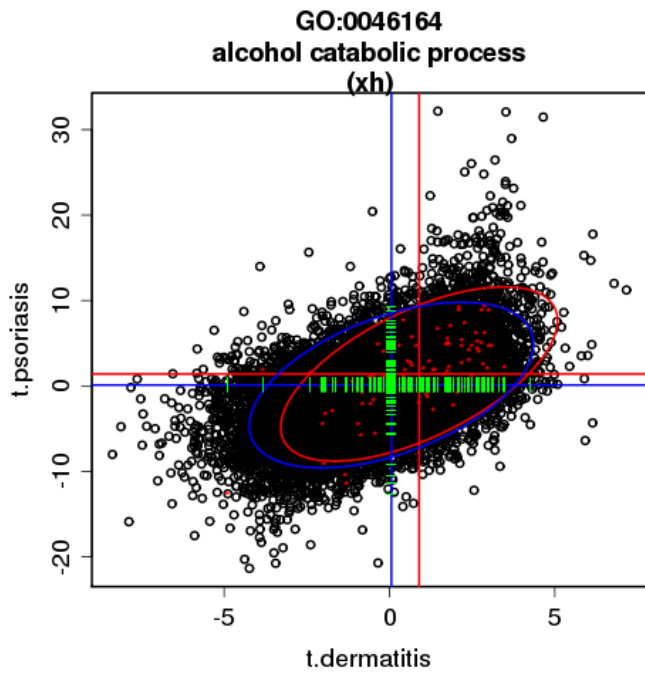
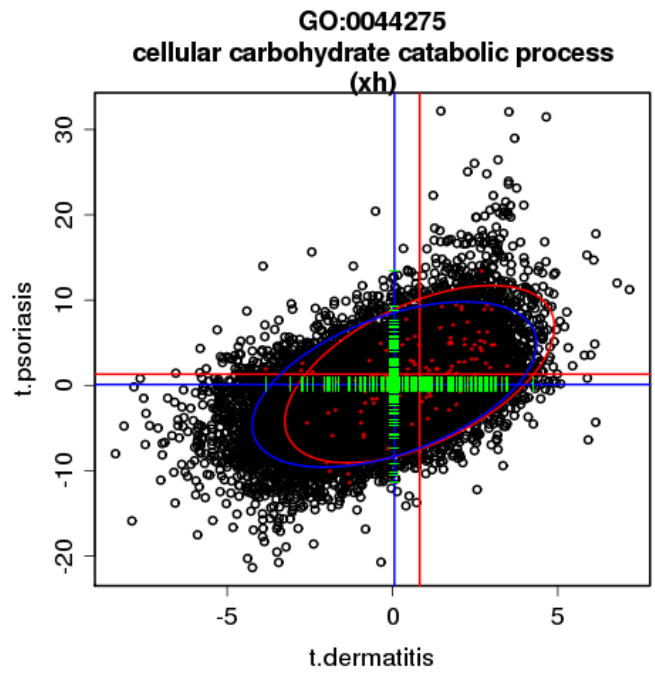
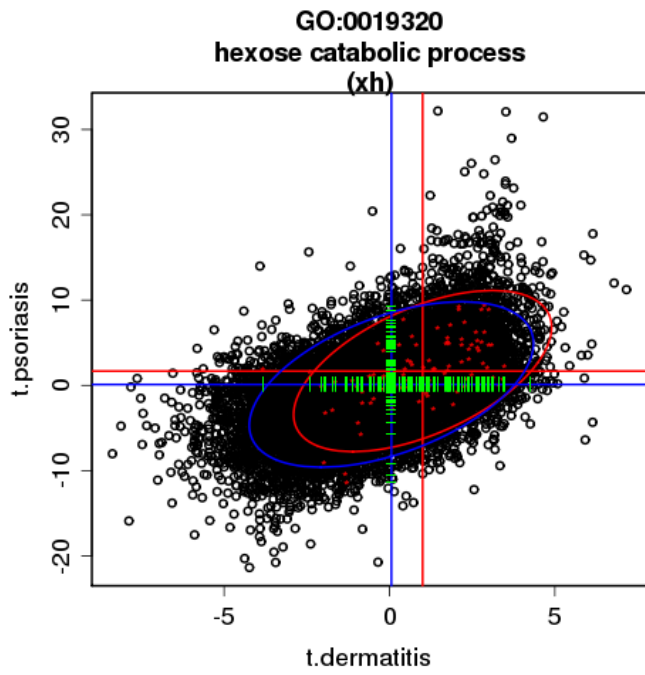


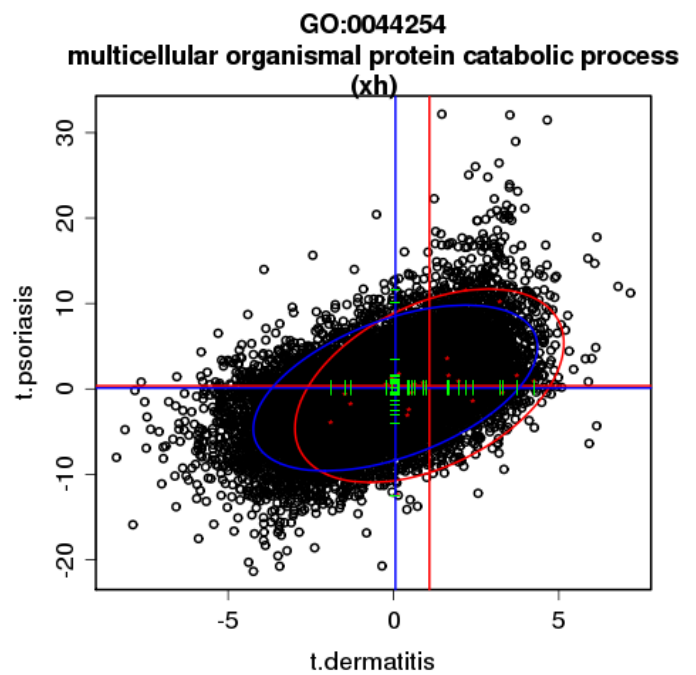
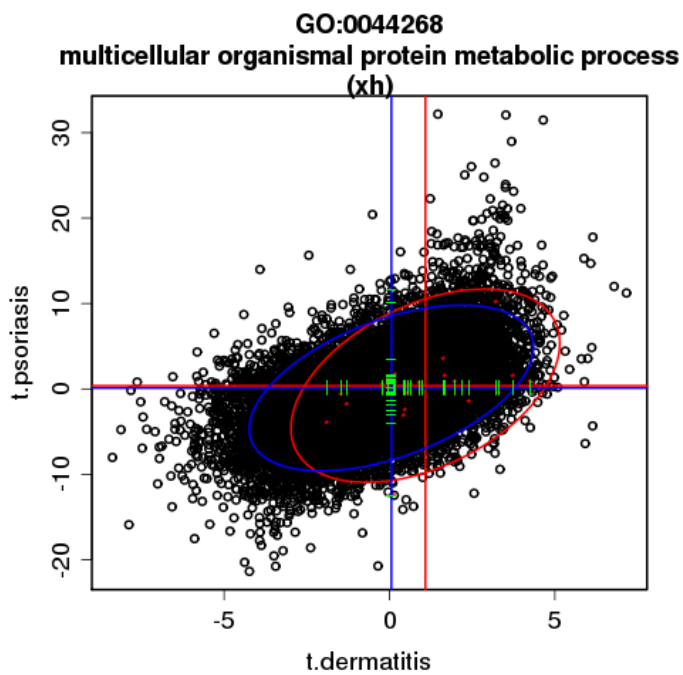
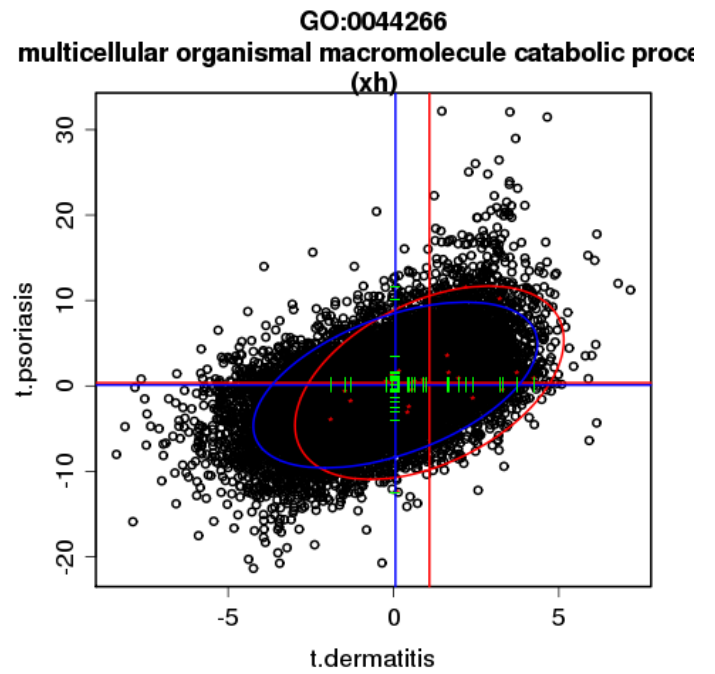
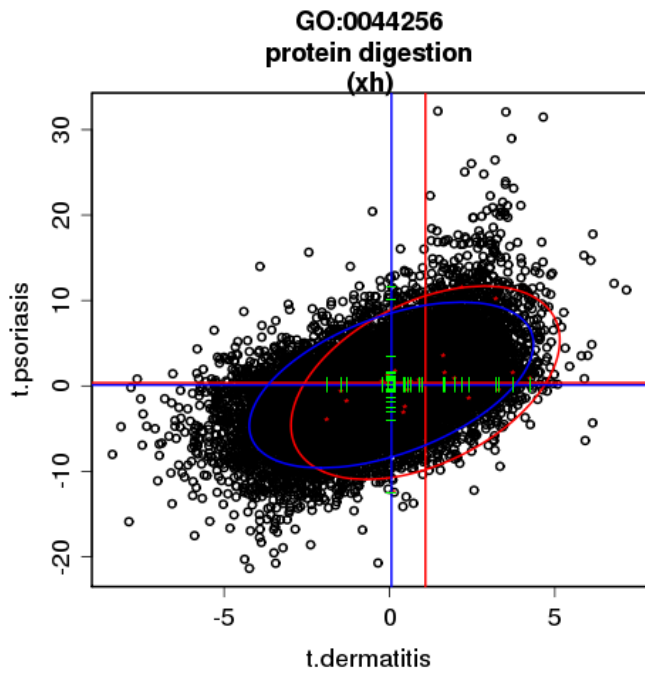
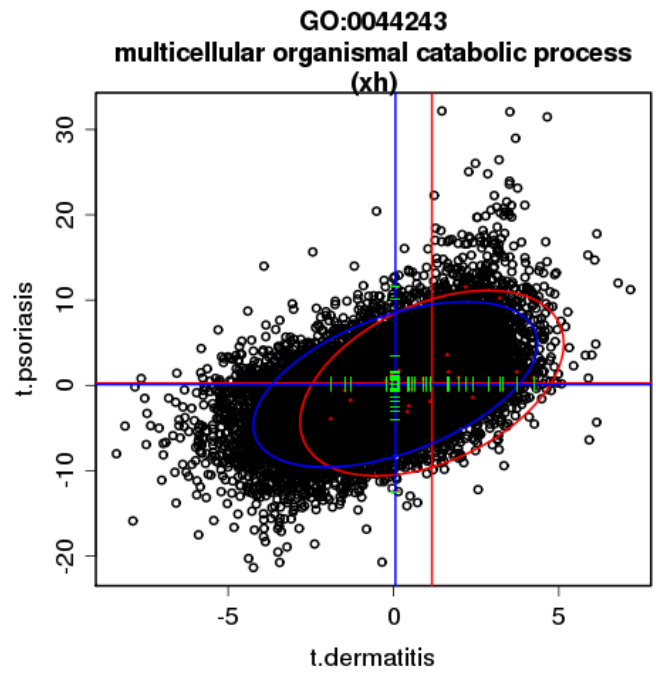
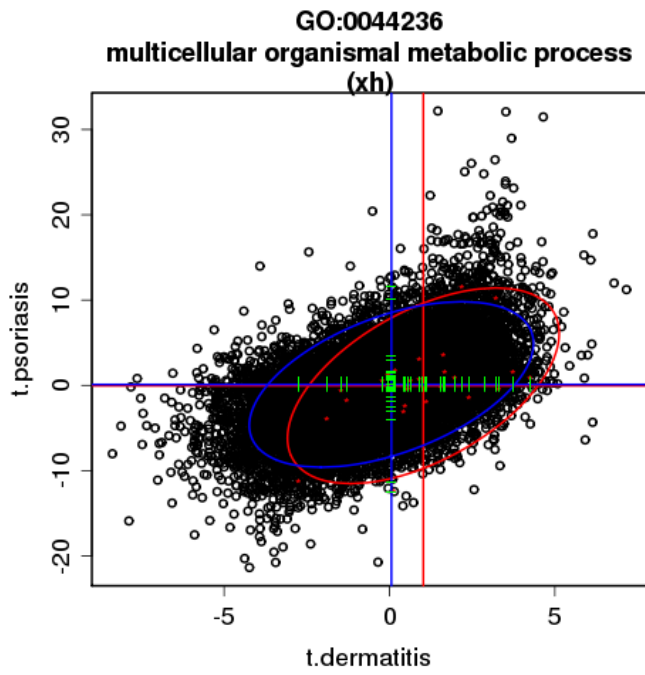
GO:0006007
glucose catabolic process
(xh)



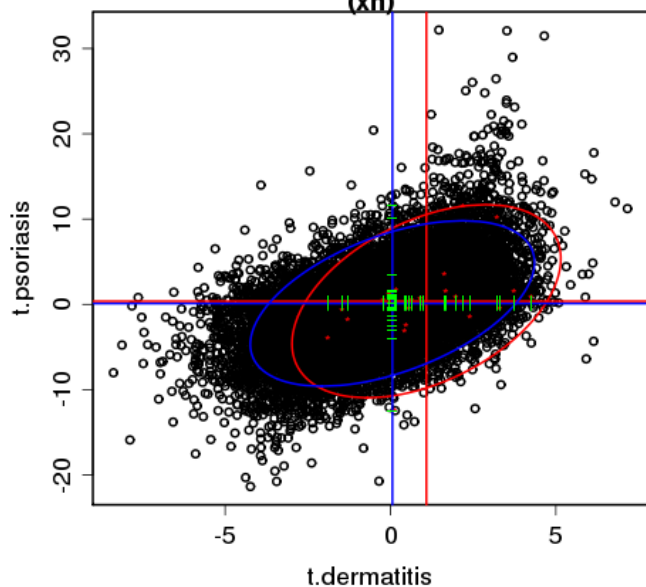
GO:0016052
carbohydrate catabolic process
(xh)



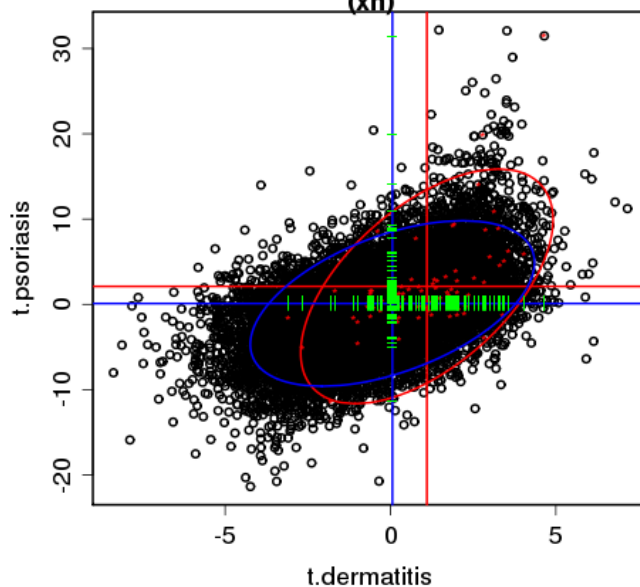




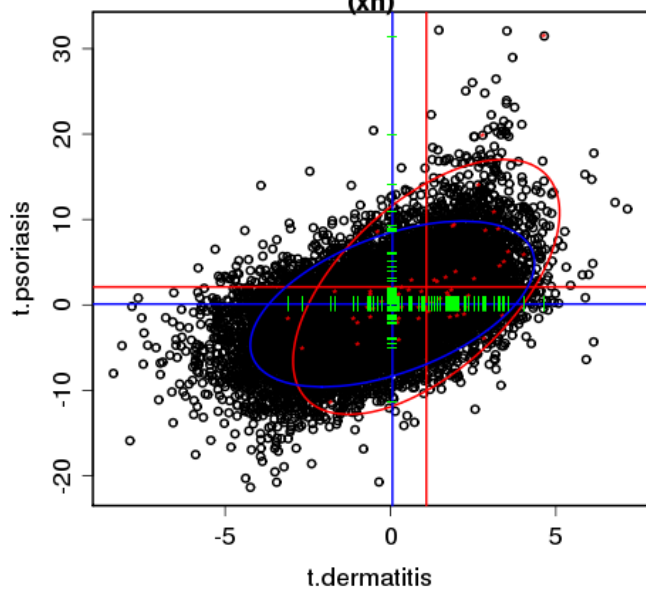
GO:0030574
collagen catabolic process
(xh)



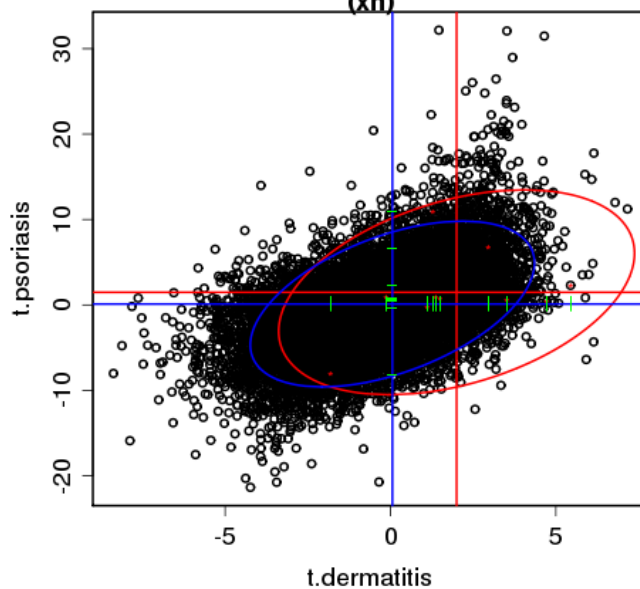
GO:0009617
response to bacterium
(xh)



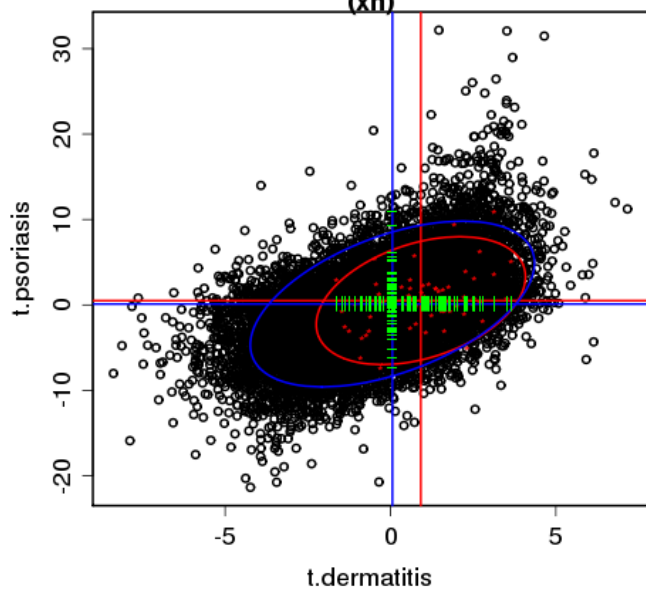
GO:0042742
defense response to bacterium
(xh)



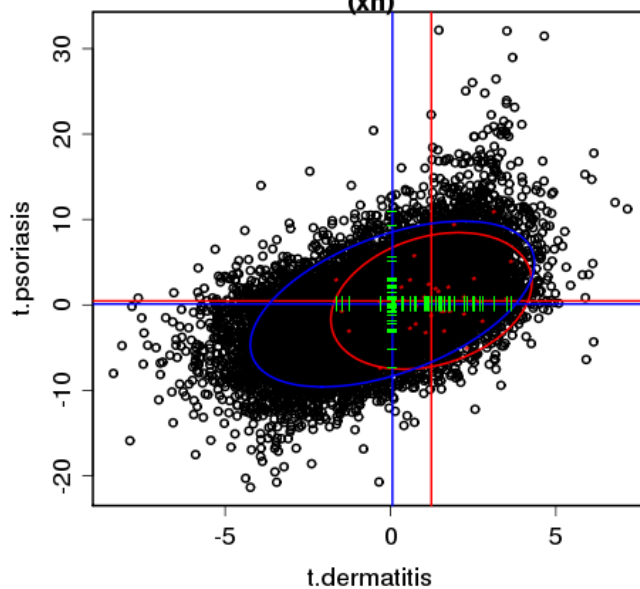
GO:0043010
camera-type eye development
(xh)



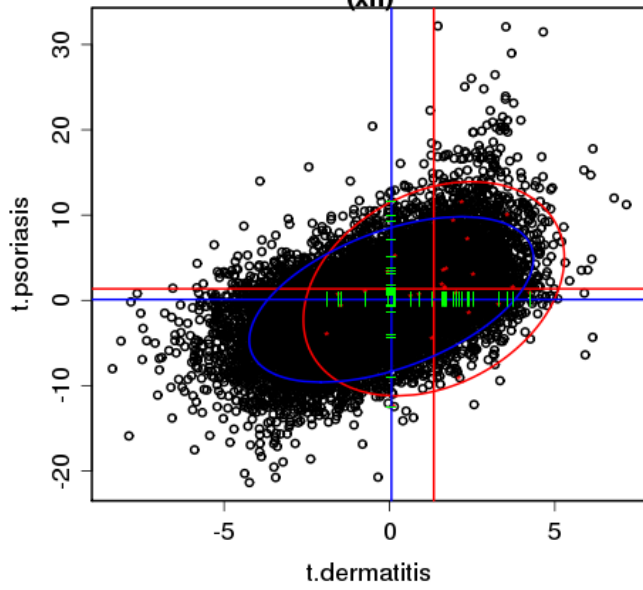
GO:0051606
detection of stimulus
(xh)



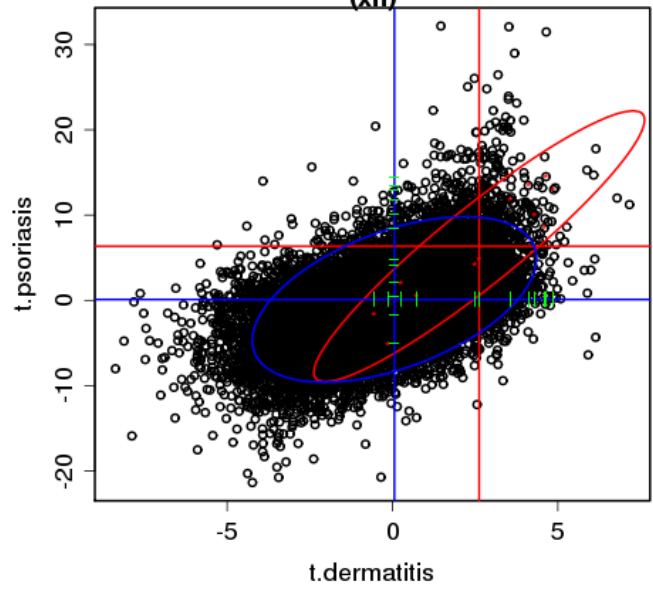
GO:0009581
detection of external stimulus
(xh)



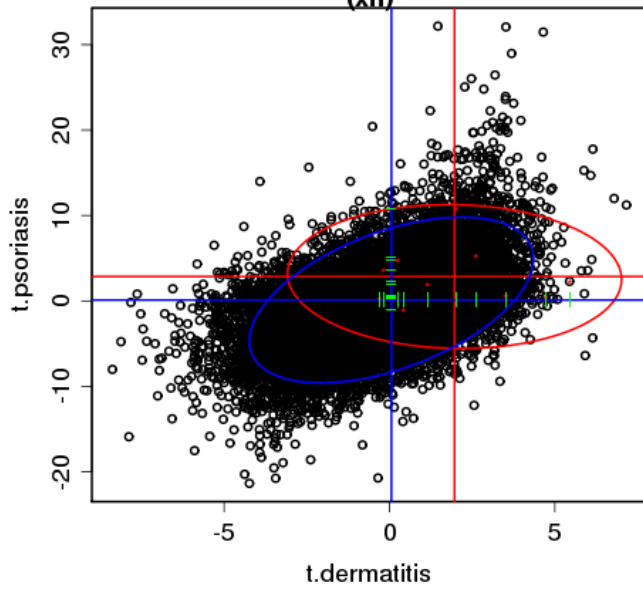
GO:0000270
peptidoglycan metabolic process
(xh)



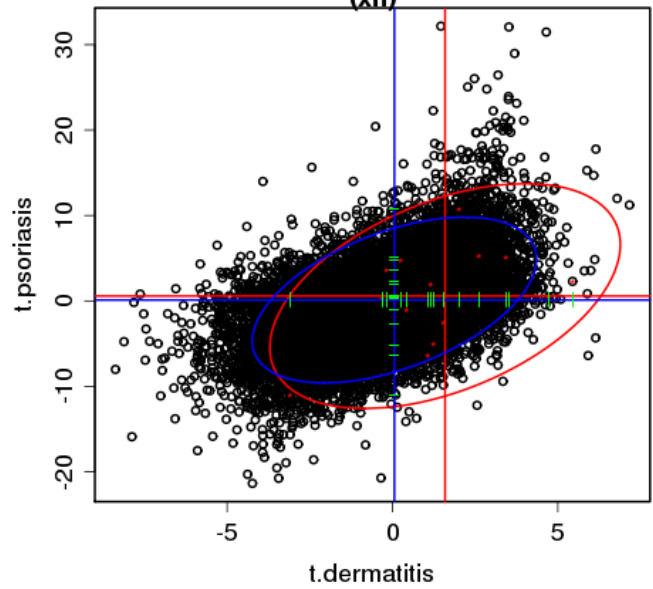
GO:0043542
endothelial cell migration
(xh)



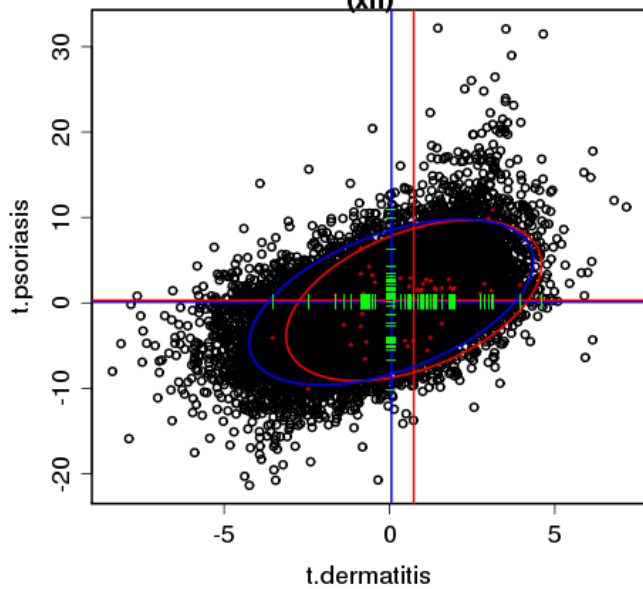
GO:0051208
sequestering of calcium ion
(xh)



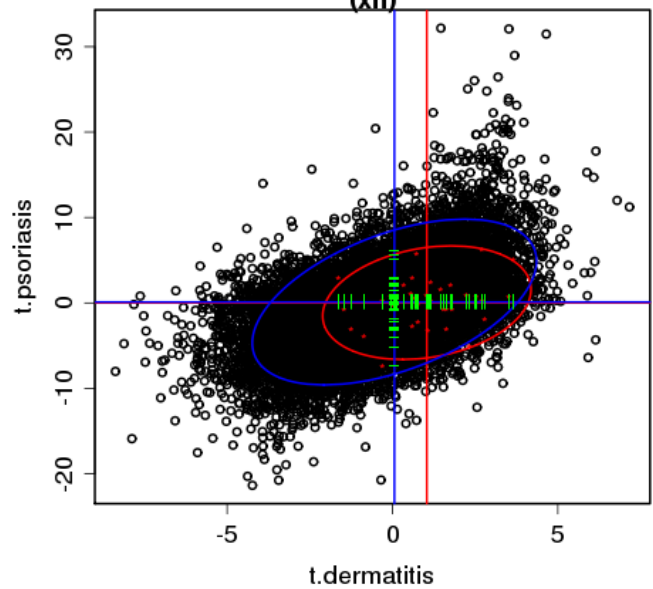
GO:0051238
sequestering of metal ion
(xh)

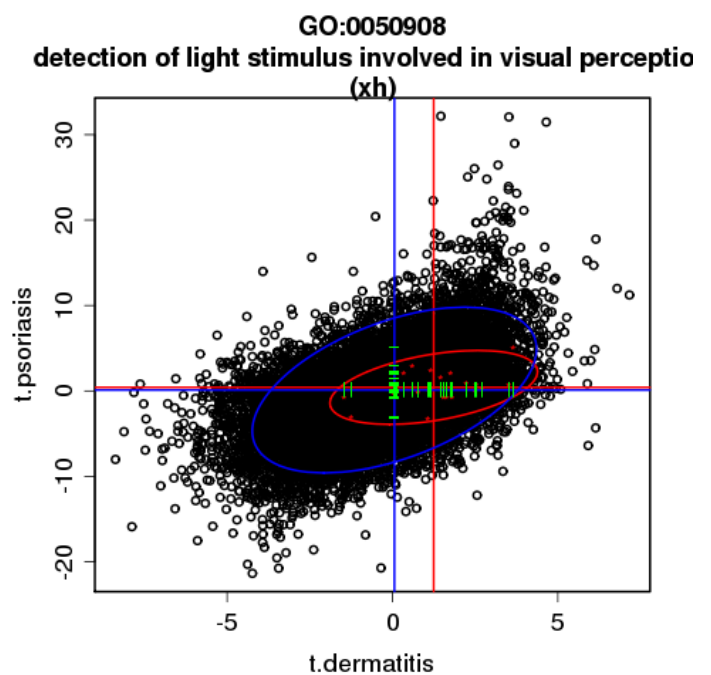
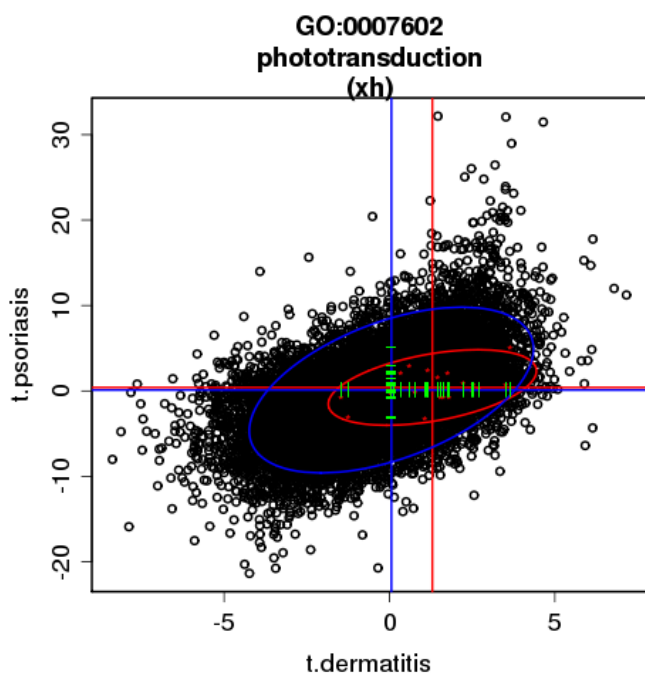
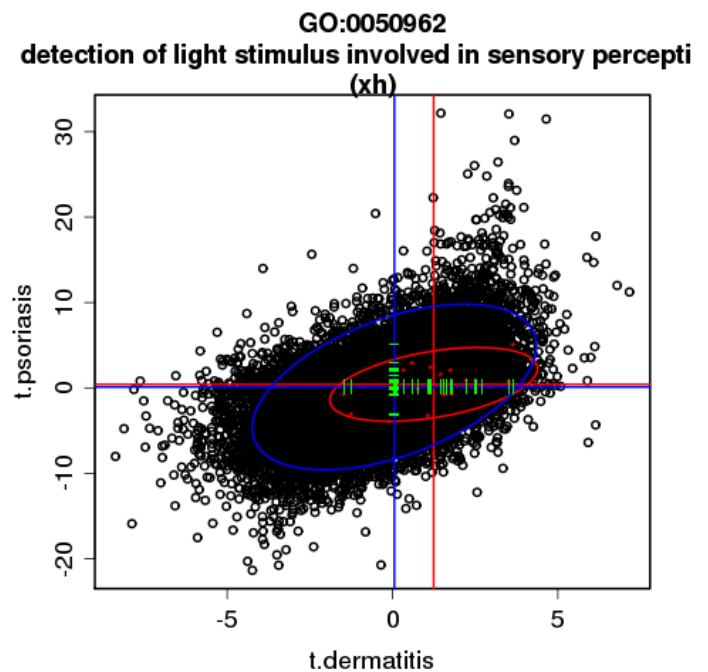
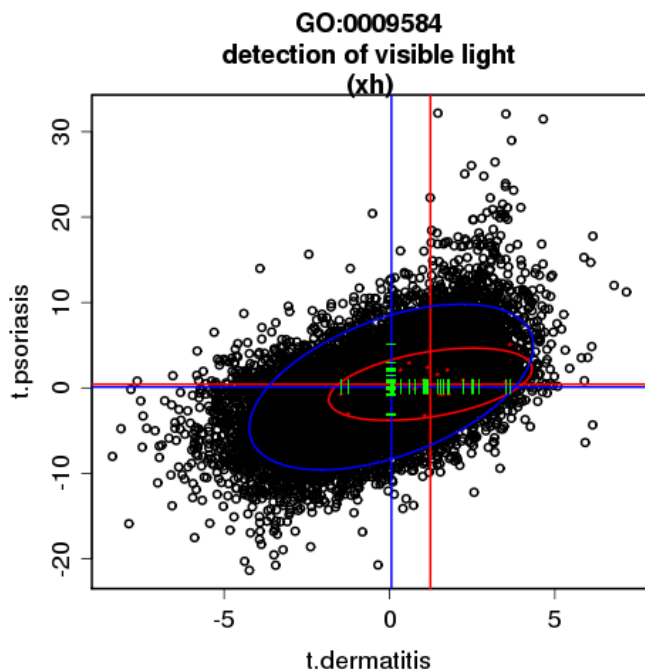
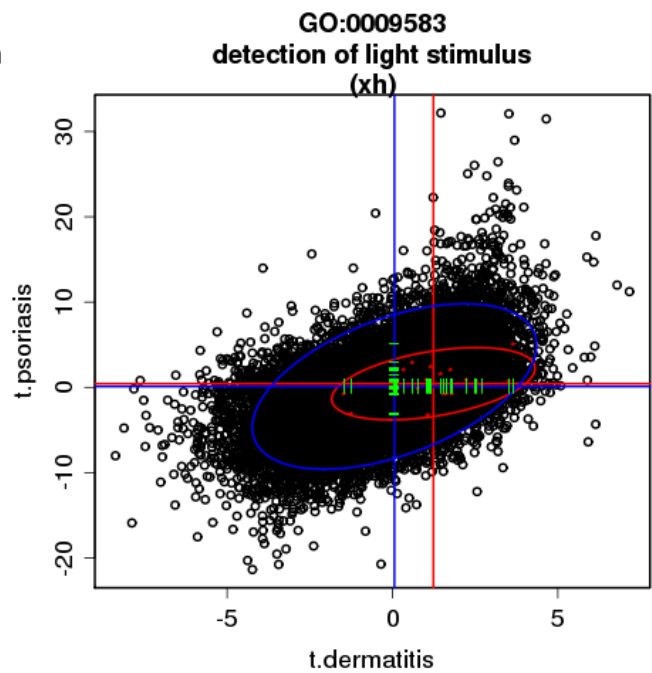
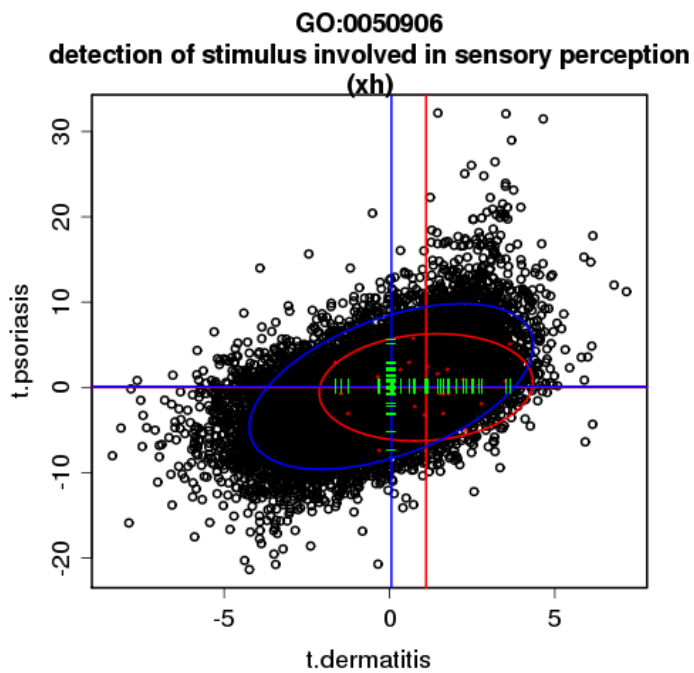


GO:0009306
protein secretion
(xh)

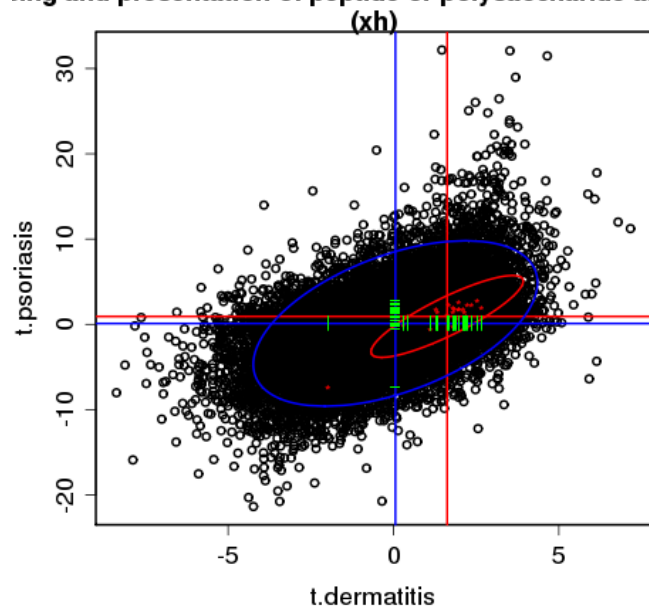


GO:0009582
detection of abiotic stimulus
(xh)

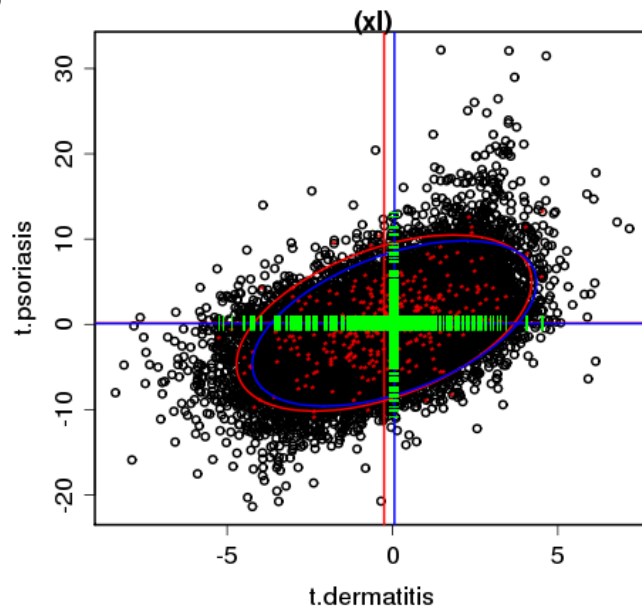




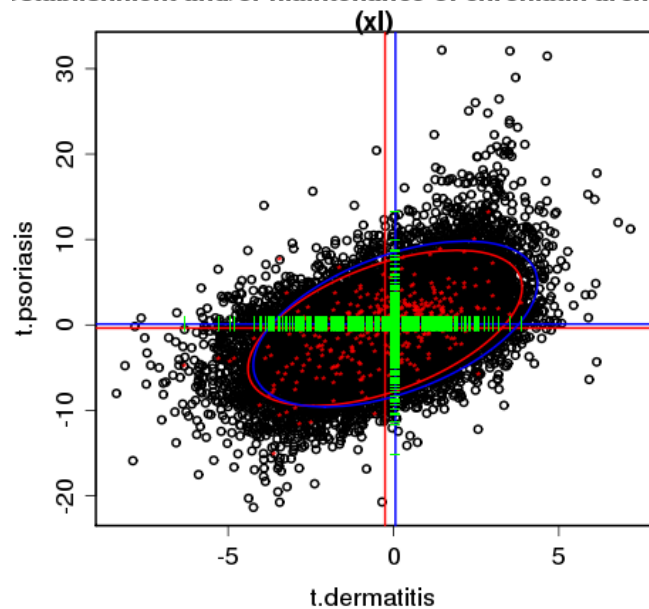
GO:0002504
antigen presentation and presentation of peptide or polysaccharide antigen



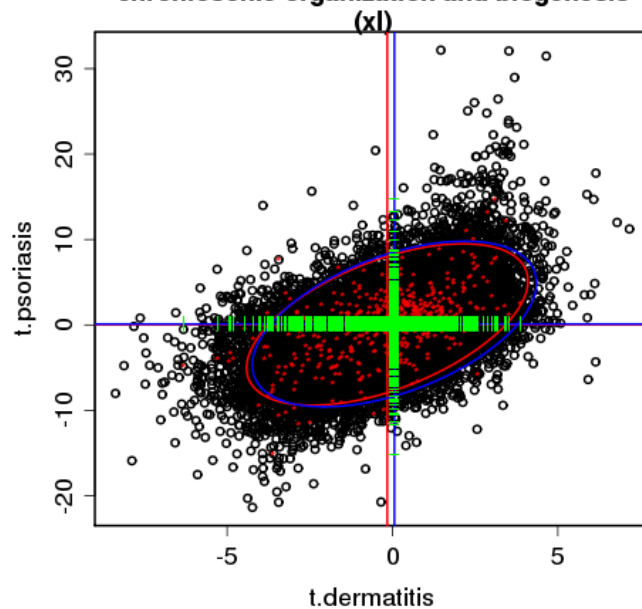
GO:0045045



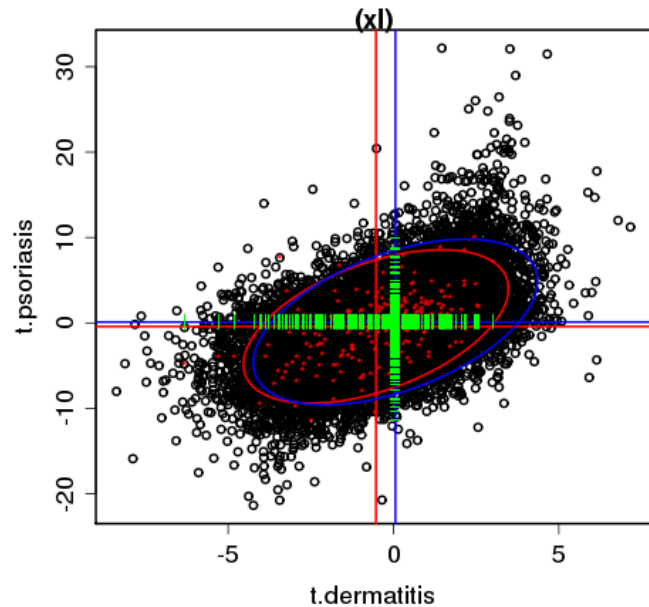
GO:0006325
chromatin organization and/or maintenance of chromatin architecture



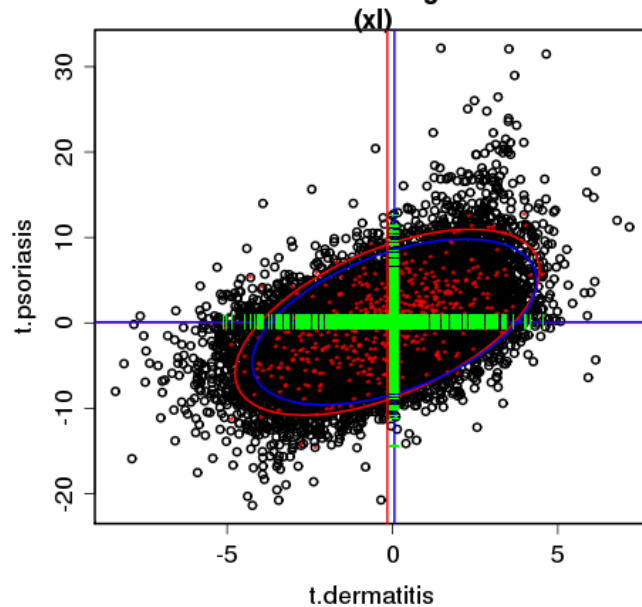
GO:0051276
chromosome organization and biogenesis



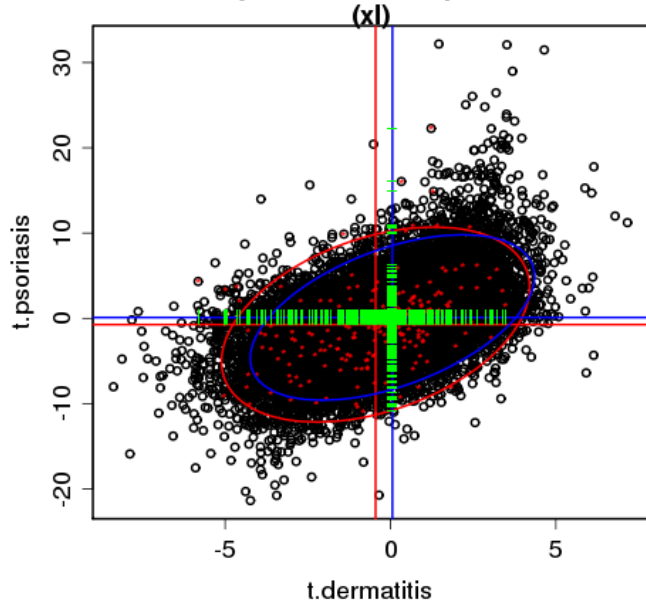
GO:0016568
chromatin modification



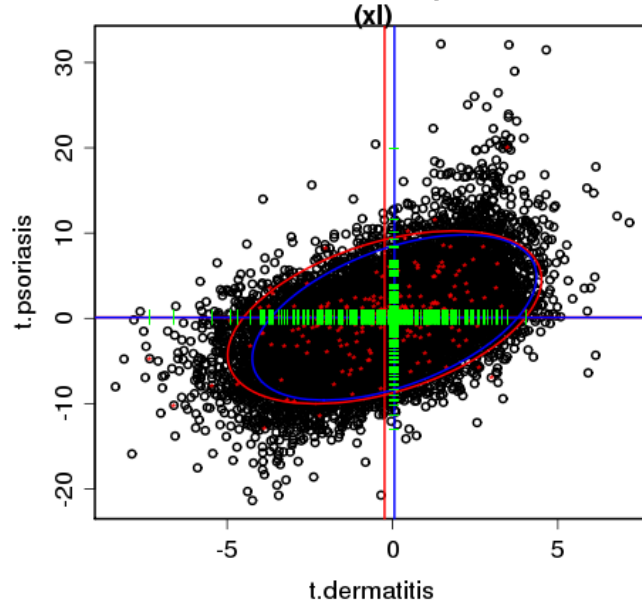
GO:0007264
small GTPase mediated signal transduction



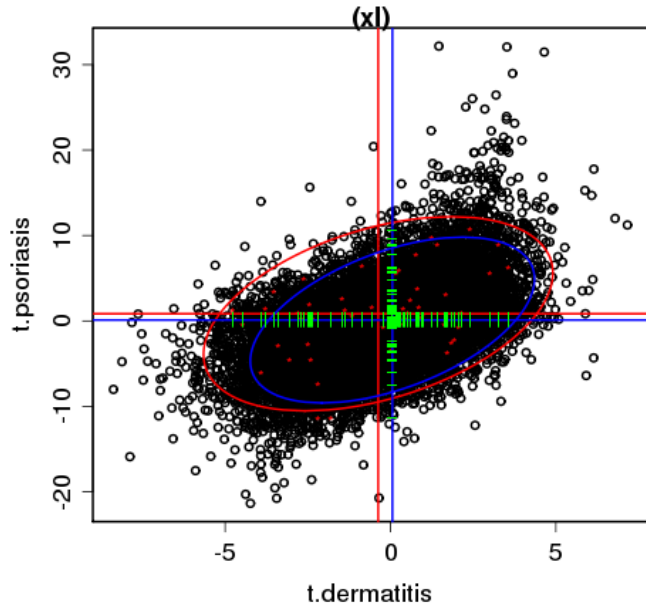
GO:0006631
fatty acid metabolic process



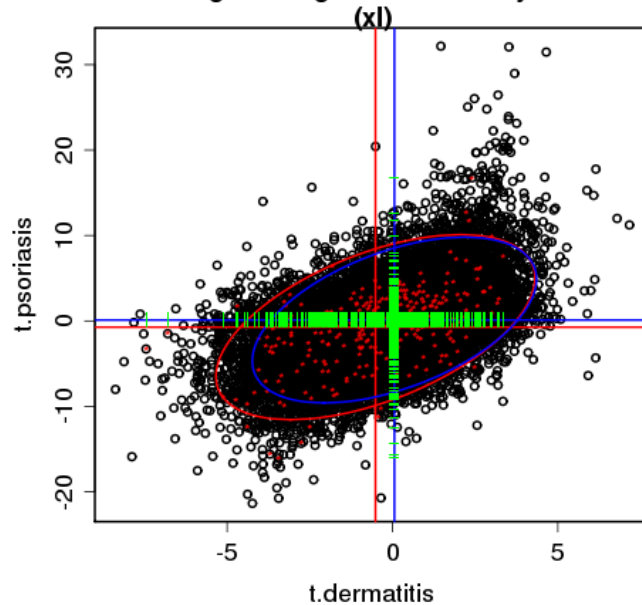
GO:0008202
steroid metabolic process



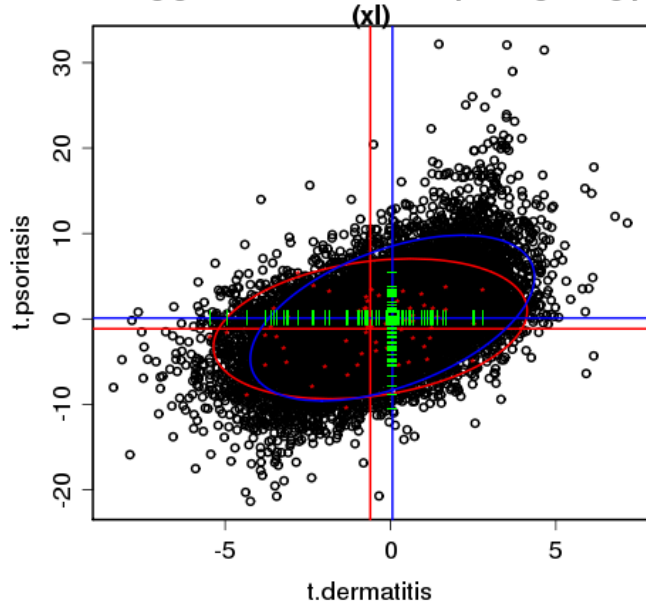
GO:0030183
B cell differentiation



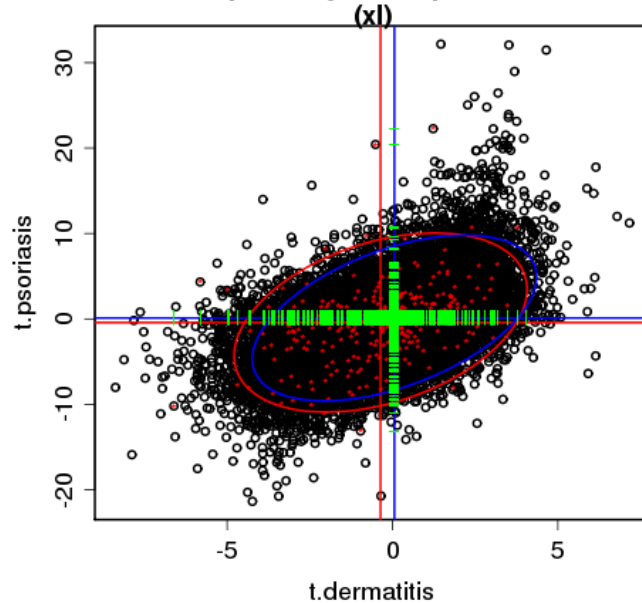
GO:0045786
negative regulation of cell cycle



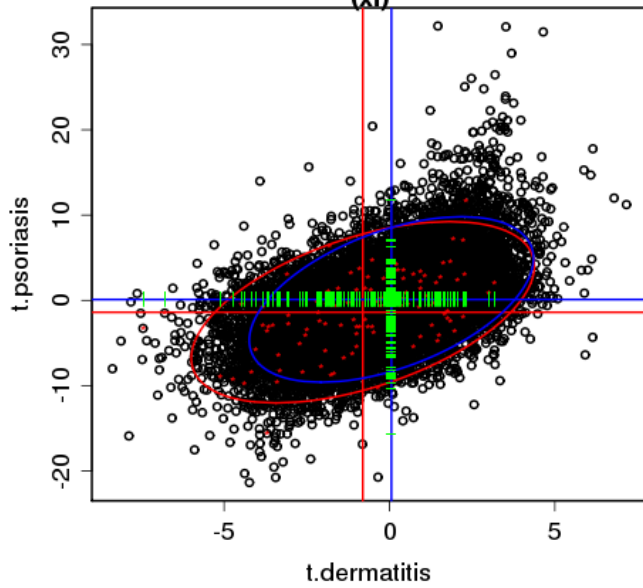
GO:0007179
transforming growth factor beta receptor signaling pathway



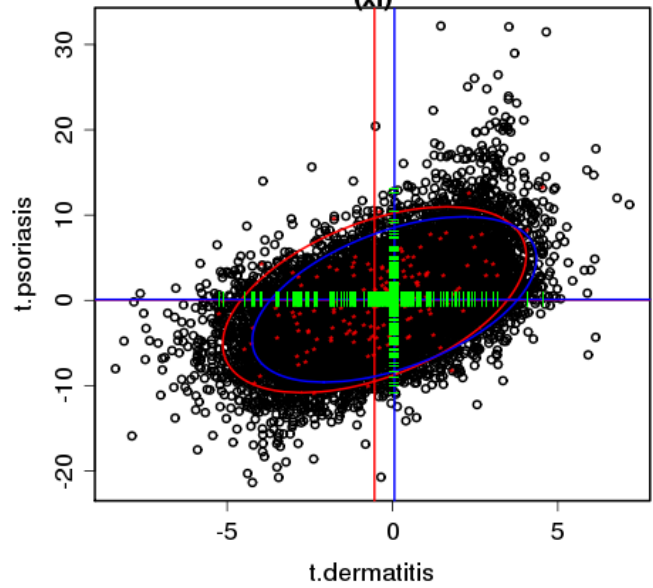
GO:0008610
lipid biosynthetic process



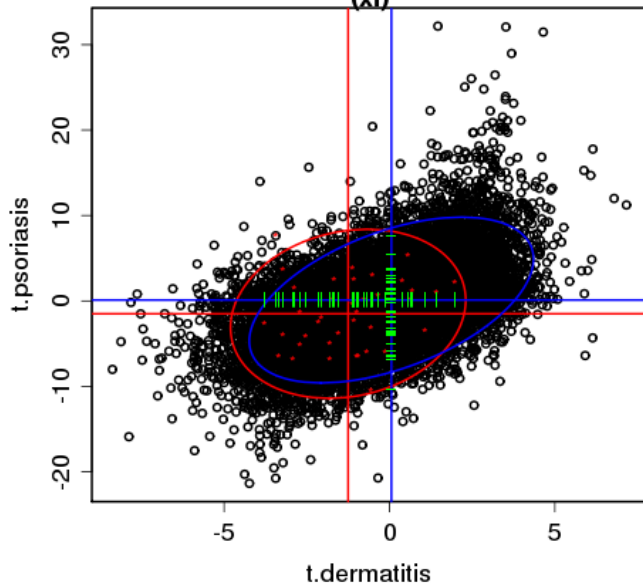
GO:0007050
cell cycle arrest
(xl)



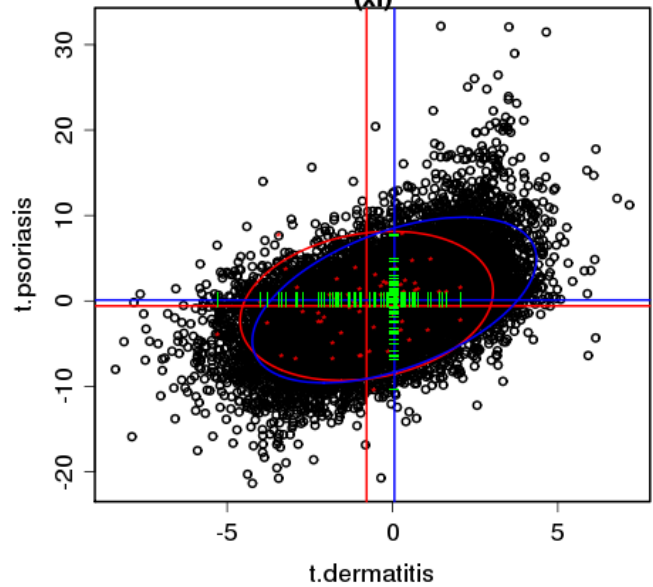
GO:0048193
Golgi vesicle transport
(xl)



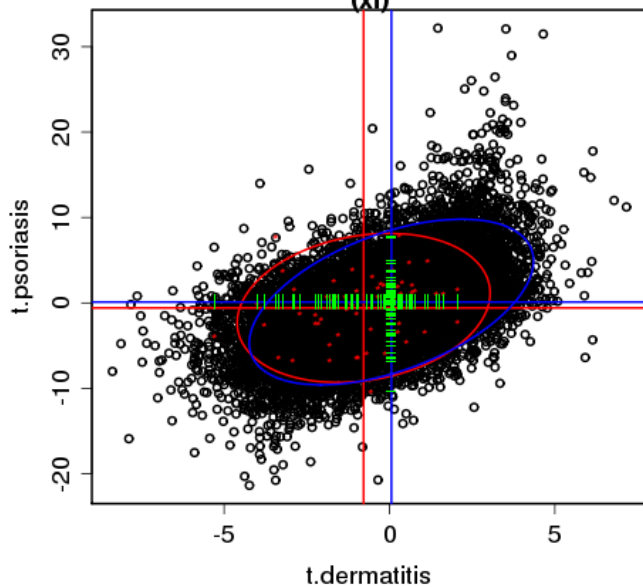
GO:0006473
protein amino acid acetylation
(xl)



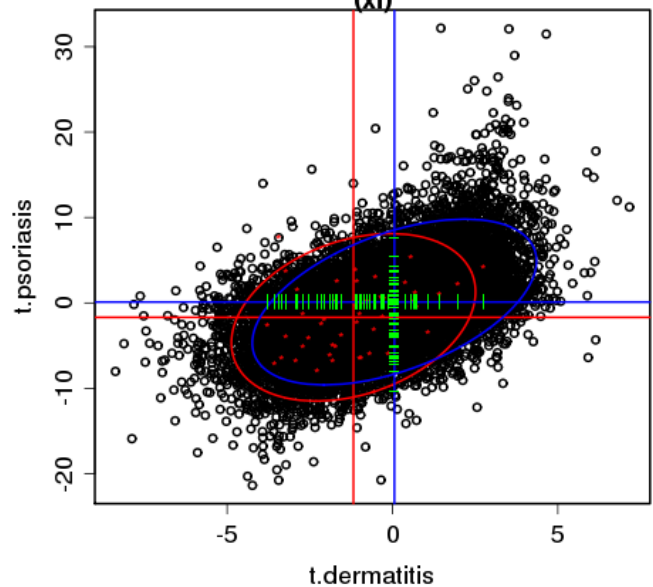
GO:0016569
covalent chromatin modification
(xl)



GO:0016570
histone modification
(xl)



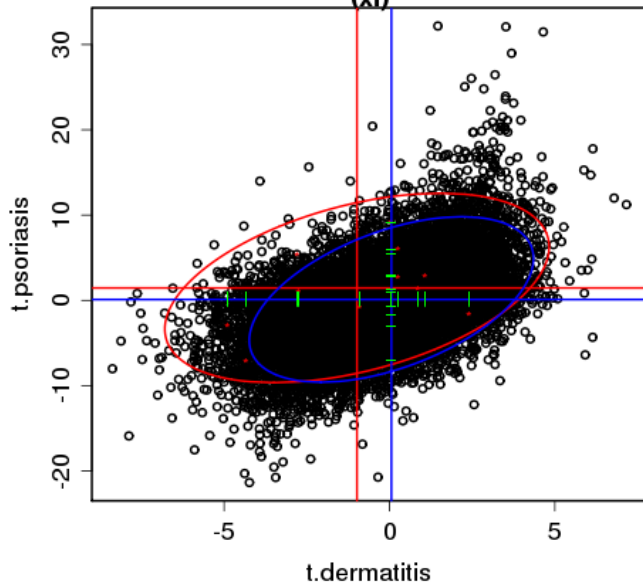
GO:0043543
protein amino acid acylation
(xl)



GO:0032273

positive regulation of protein polymerization

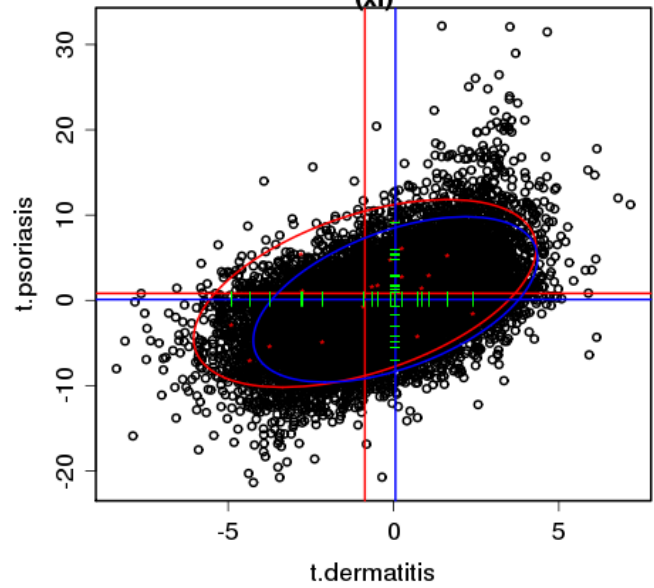
(xl)



GO:0051495

positive regulation of cytoskeleton organization and biogenesis

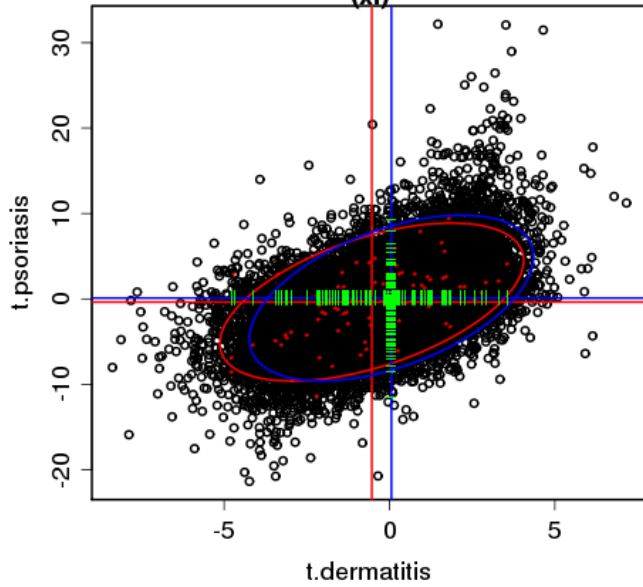
(xl)



GO:0030518

steroid hormone receptor signaling pathway

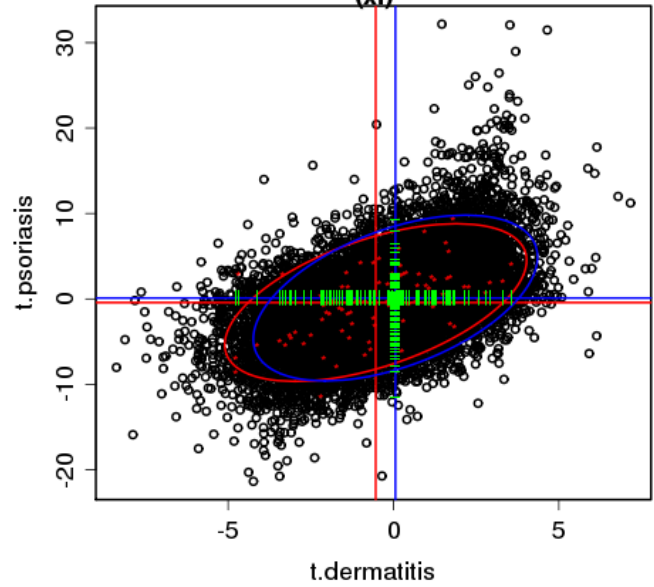
(xl)



GO:0030522

intracellular receptor-mediated signaling pathway

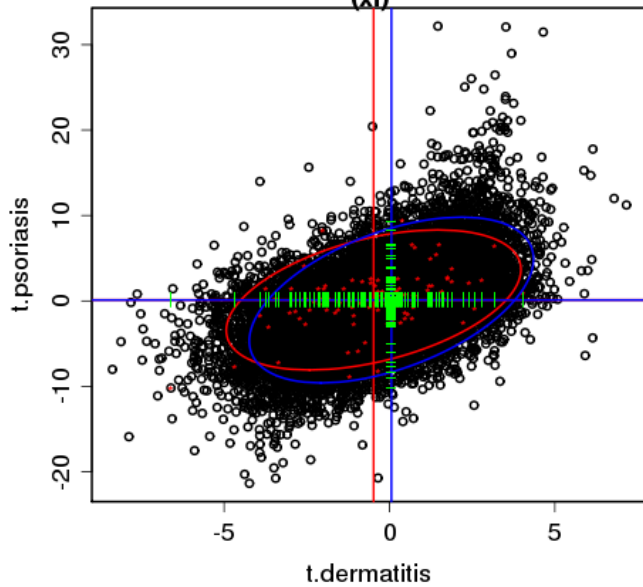
(xl)



GO:0006694

steroid biosynthetic process

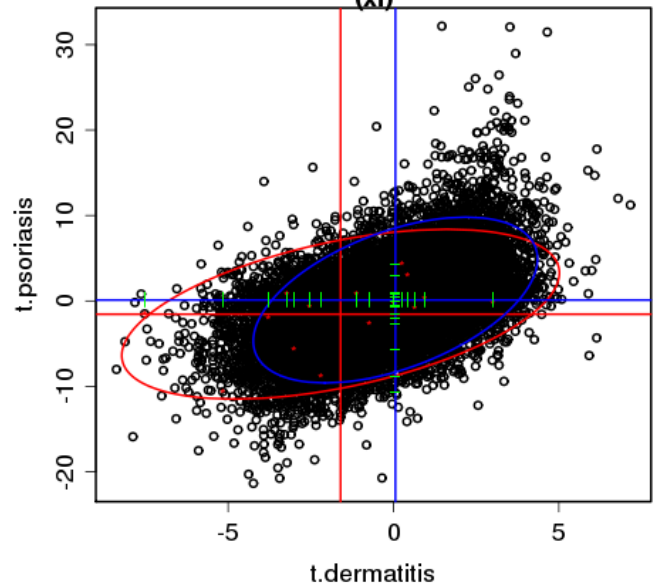
(xl)

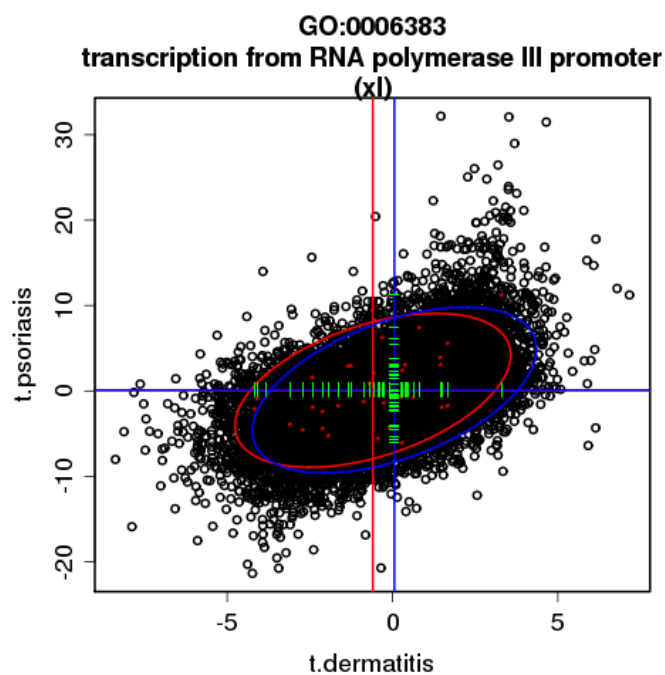
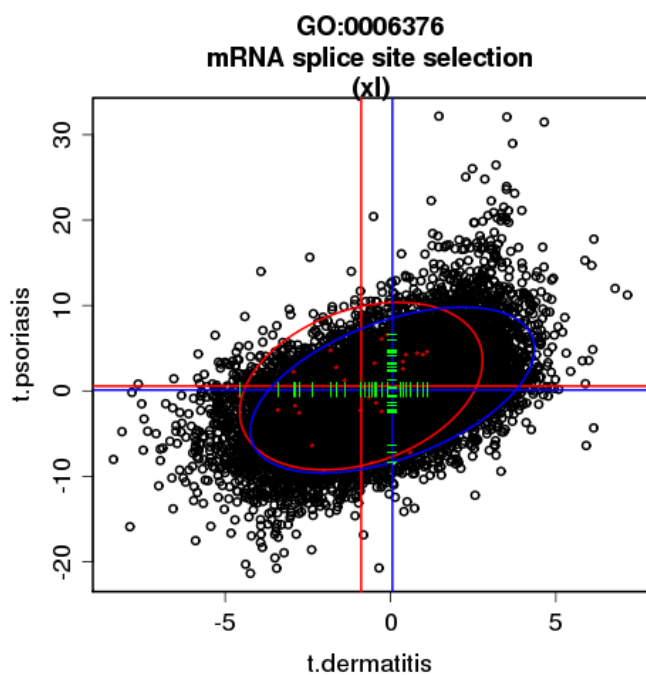
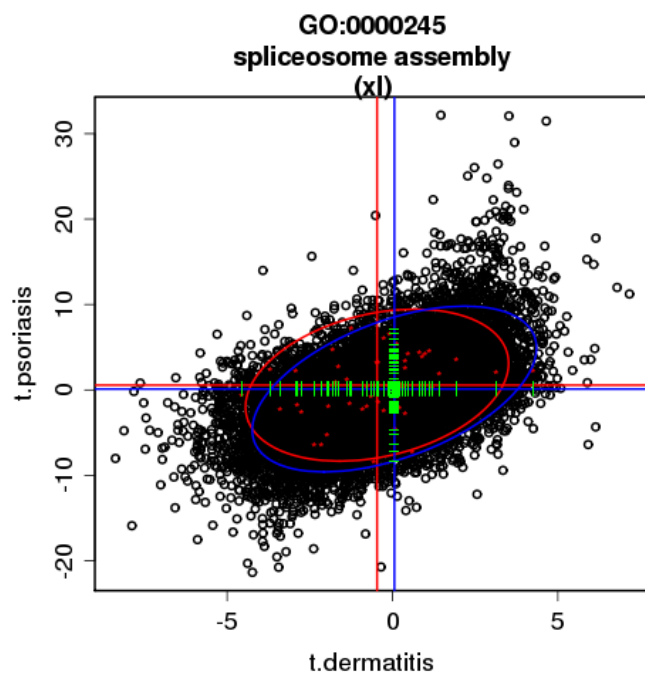
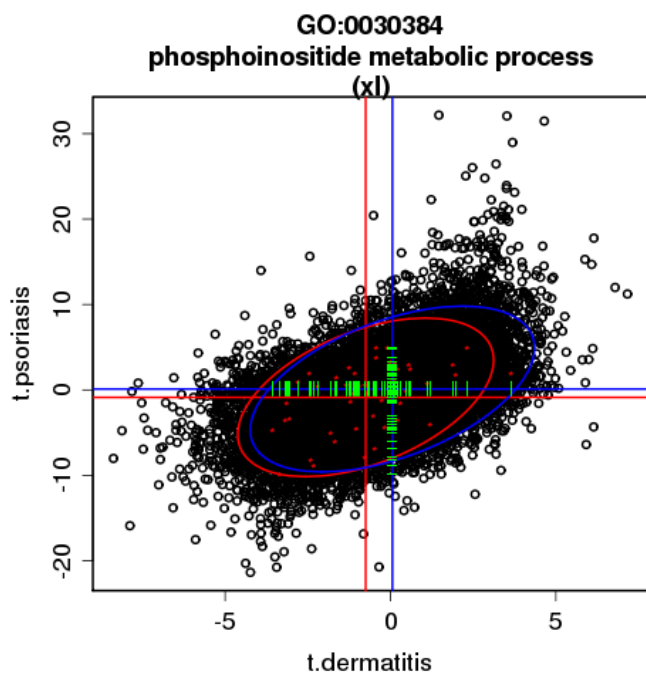
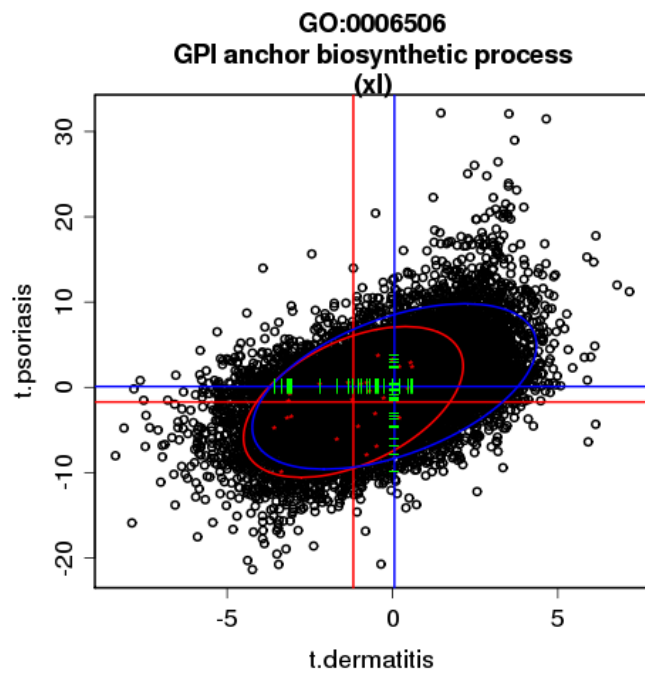
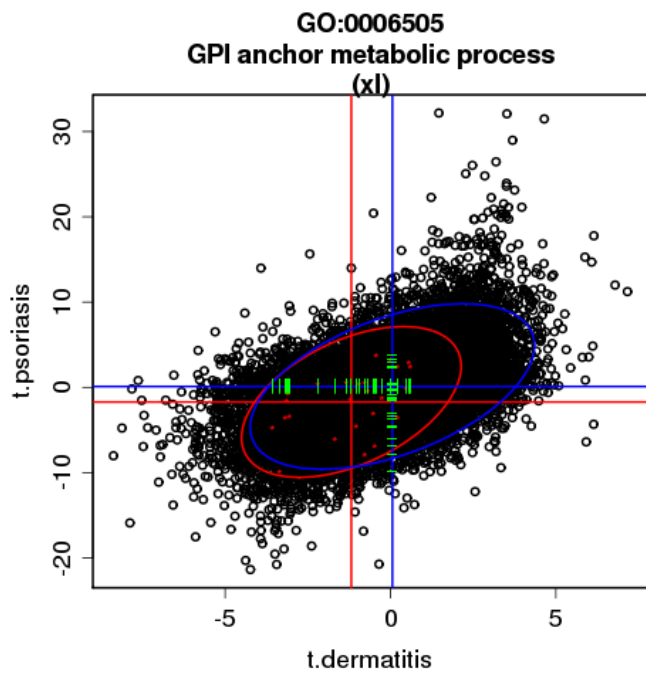


GO:0045682

regulation of epidermis development

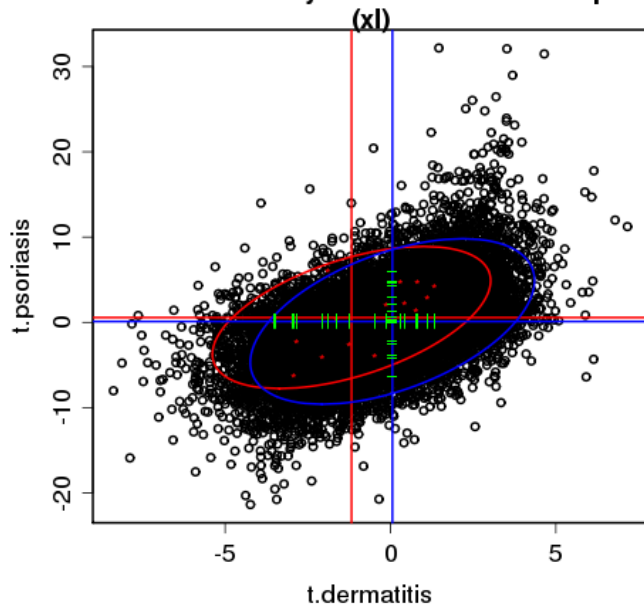
(xl)





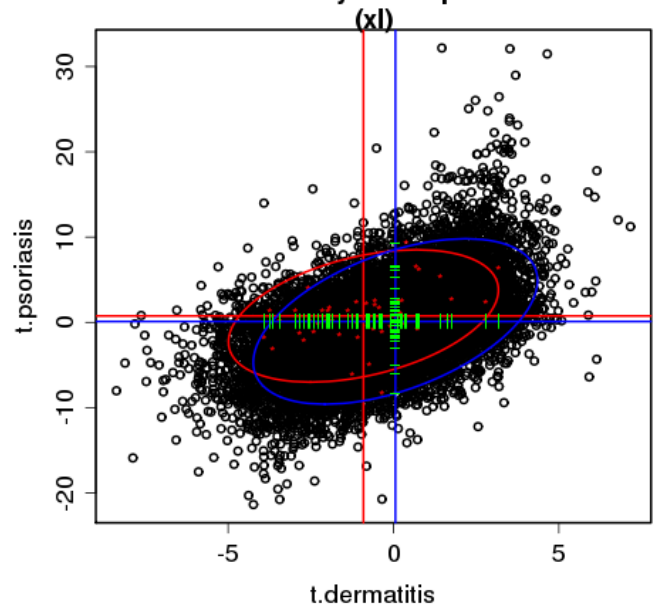
GO:0009081

branched chain family amino acid metabolic process



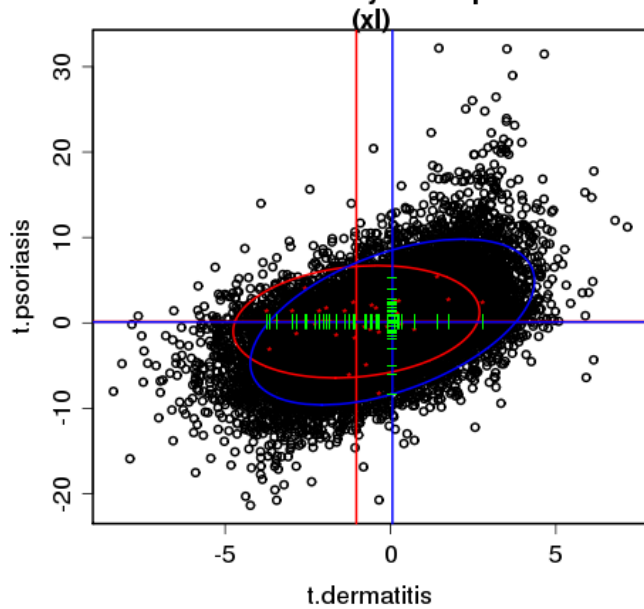
GO:0016126

sterol biosynthetic process



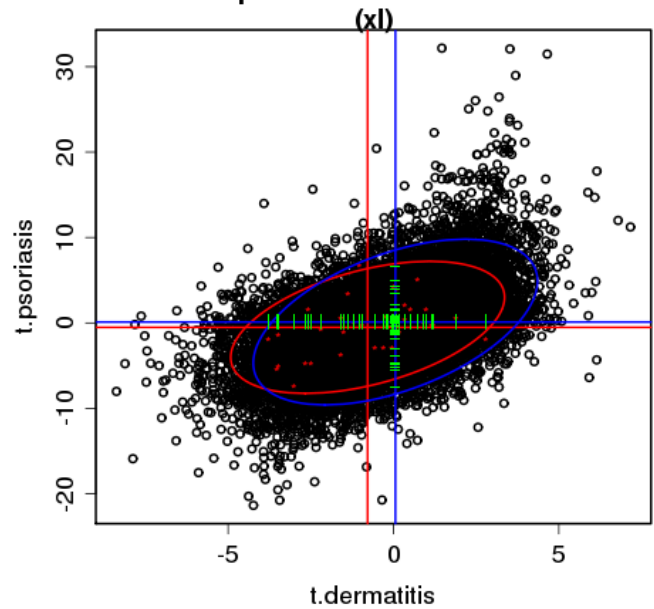
GO:0006695

cholesterol biosynthetic process



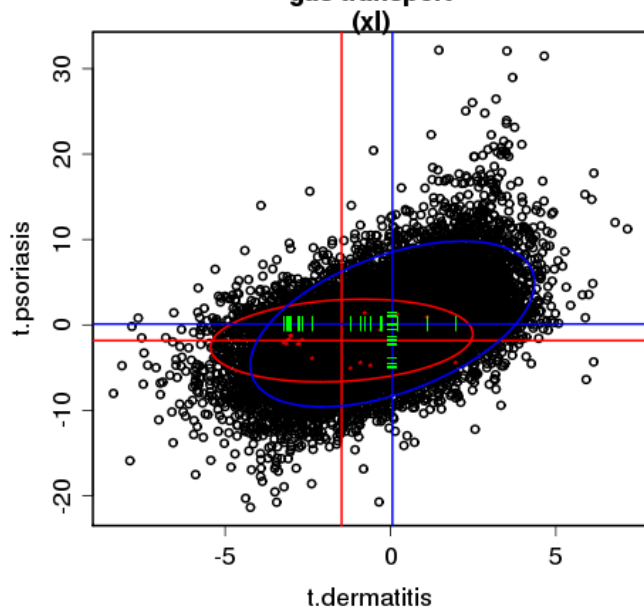
GO:0048515

spermatid differentiation



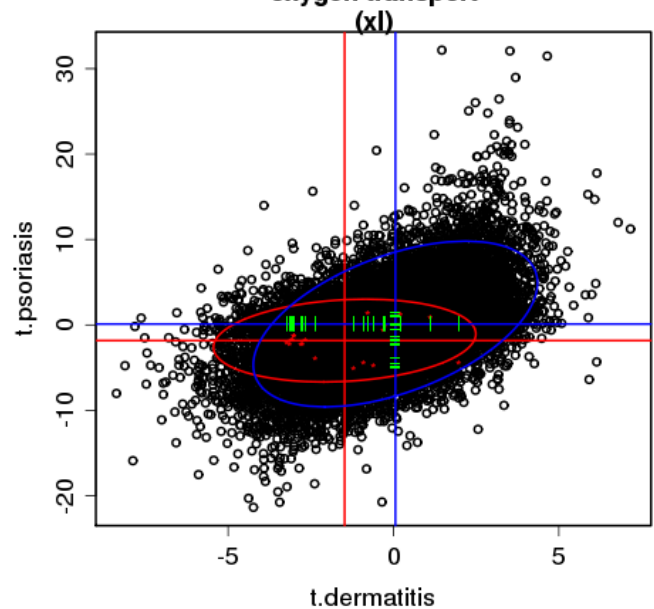
GO:0015669

gas transport

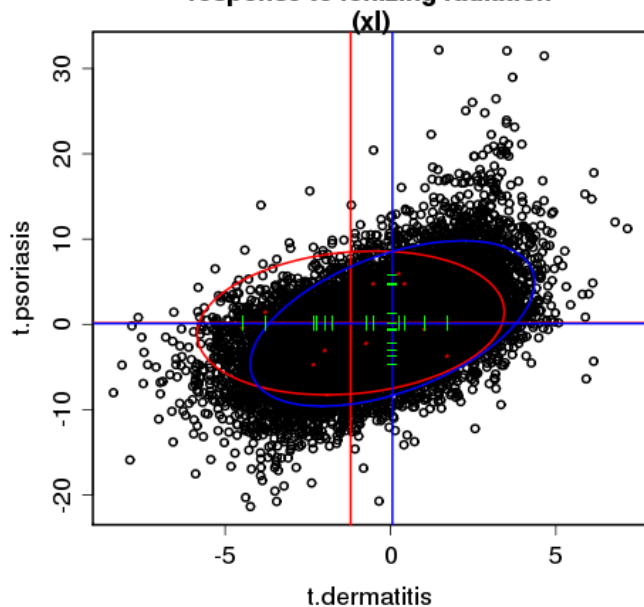


GO:0015671

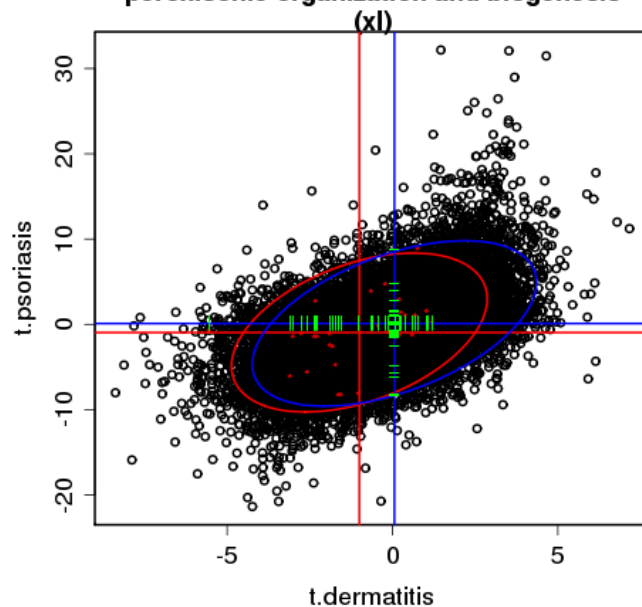
oxygen transport



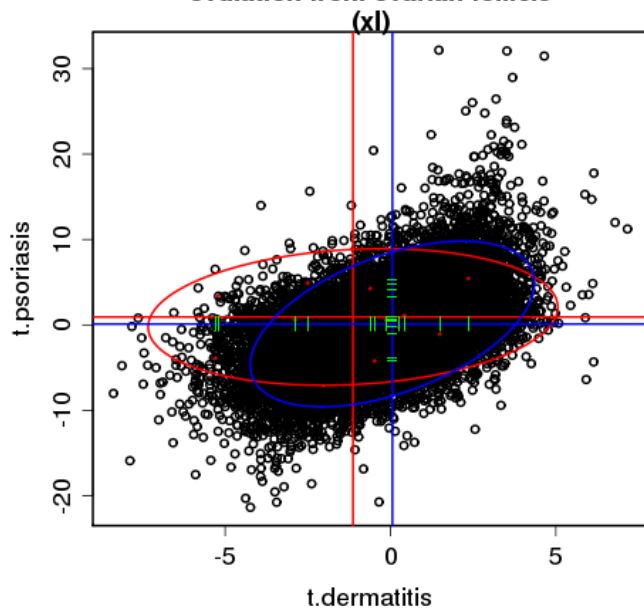
GO:0010212
response to ionizing radiation



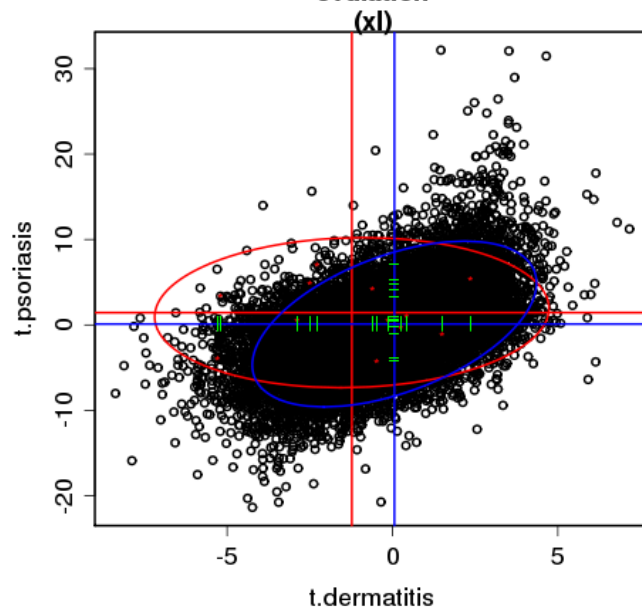
GO:0007031
peroxisome organization and biogenesis



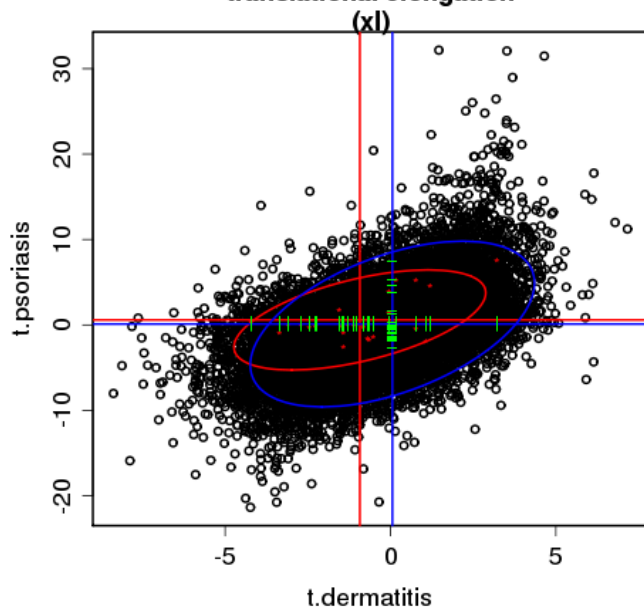
GO:0001542
ovulation from ovarian follicle



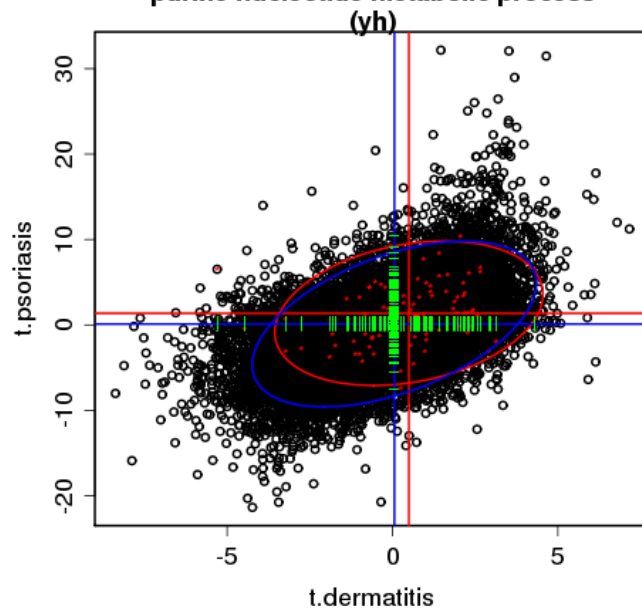
GO:0030728
ovulation



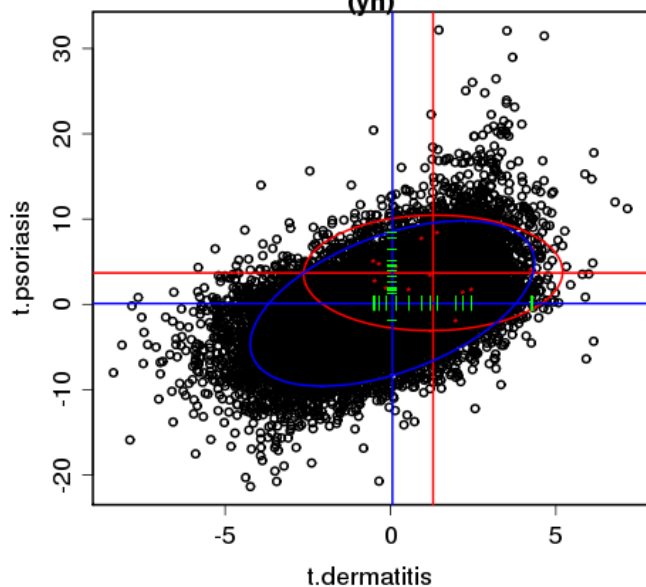
GO:0006414
translational elongation



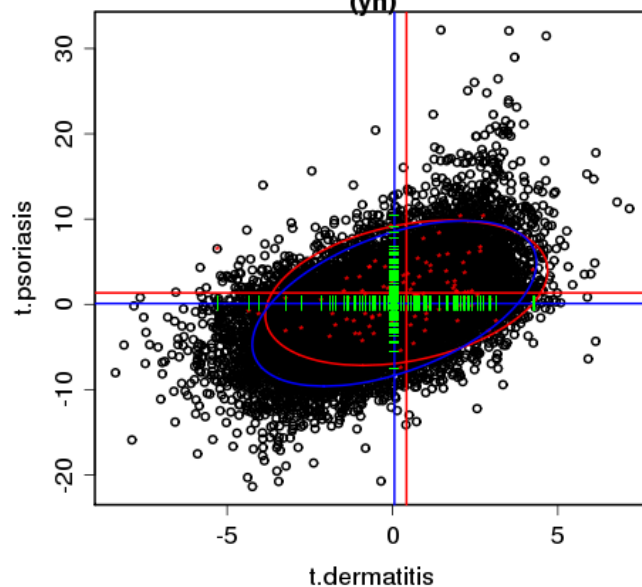
GO:0006163
purine nucleotide metabolic process



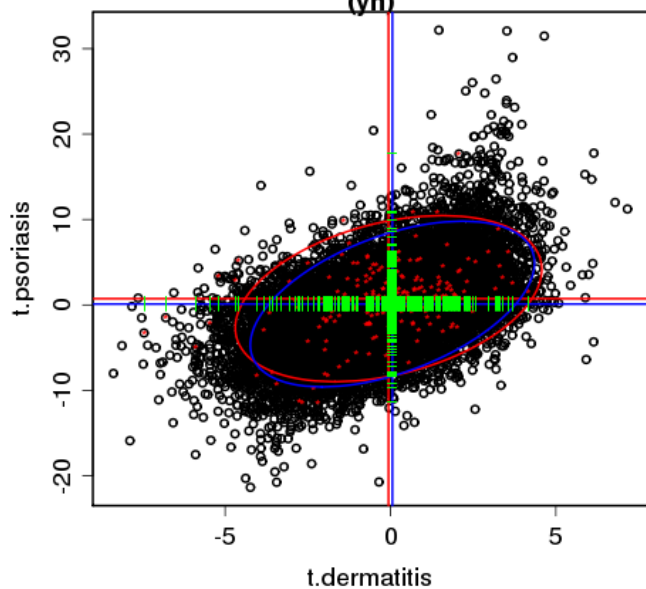
GO:0006144
purine base metabolic process
(yh)



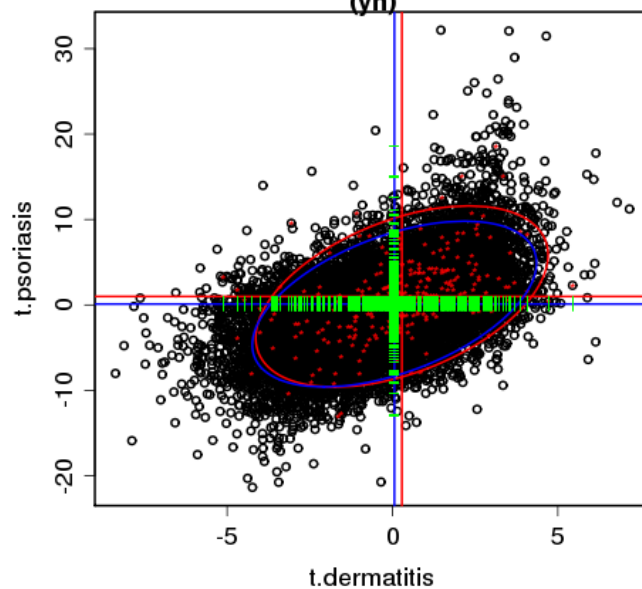
GO:0009259
ribonucleotide metabolic process
(yh)



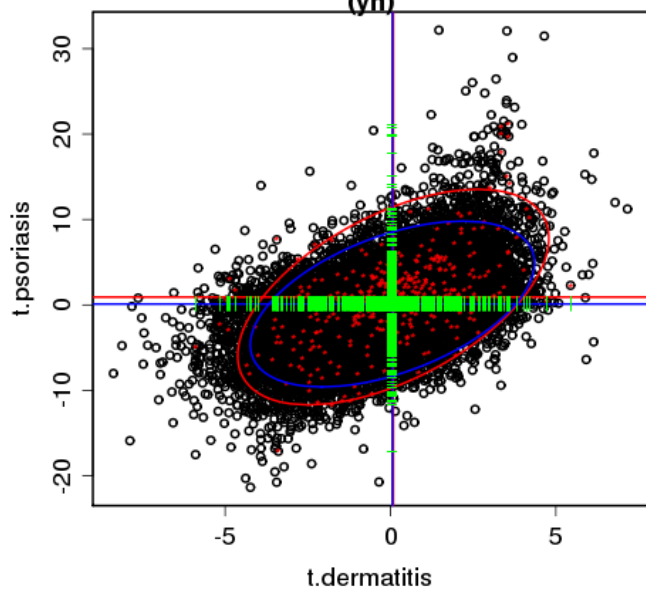
GO:0045944
positive regulation of transcription from RNA polymerase II p
(yh)



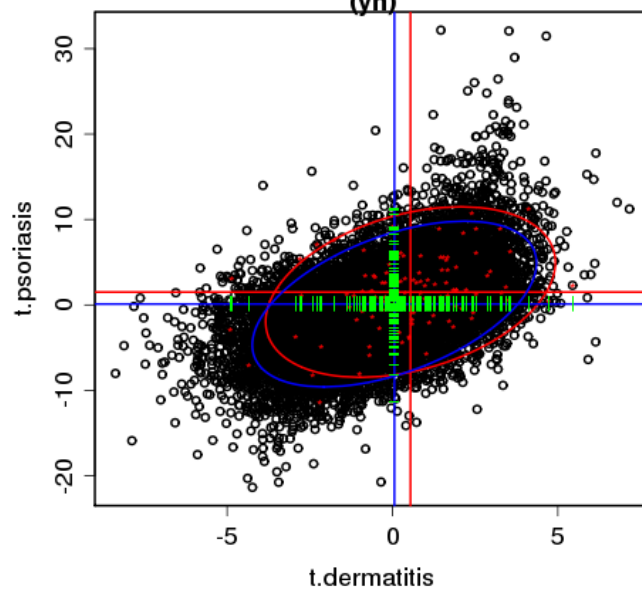
GO:0006520
amino acid metabolic process
(yh)



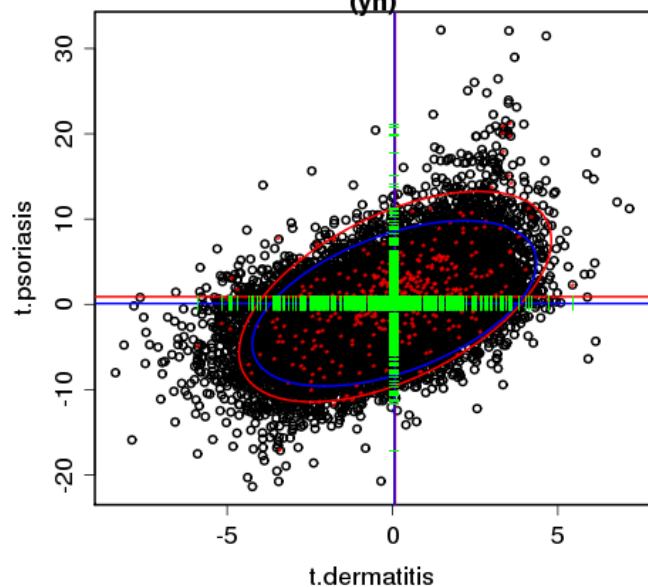
GO:0032268
regulation of cellular protein metabolic process
(yh)



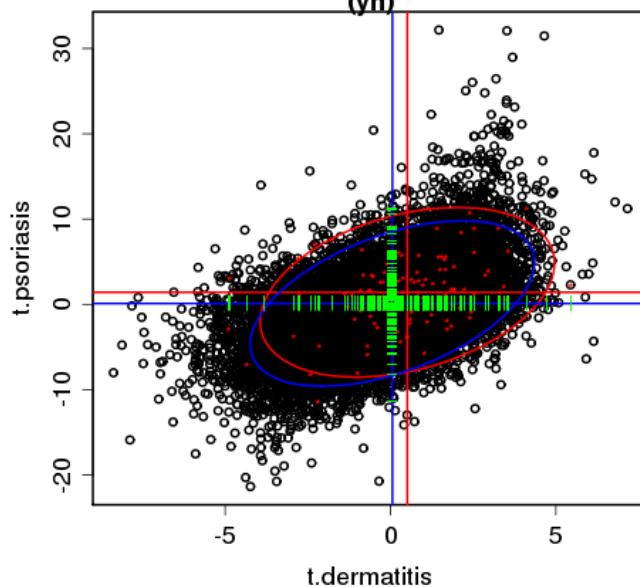
GO:0032270
positive regulation of cellular protein metabolic process
(yh)



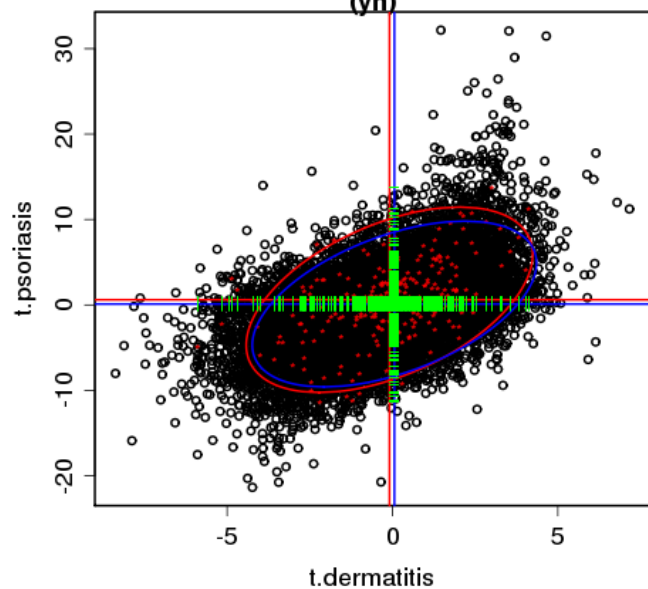
GO:0051246
regulation of protein metabolic process
(yh)



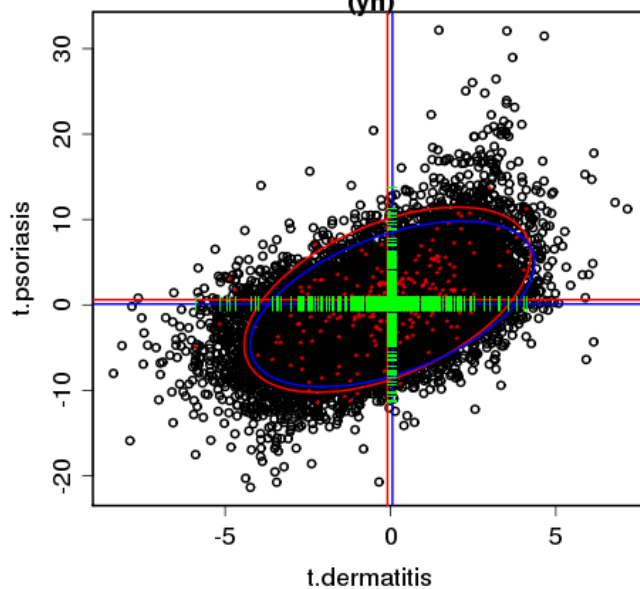
GO:0051247
positive regulation of protein metabolic process
(yh)



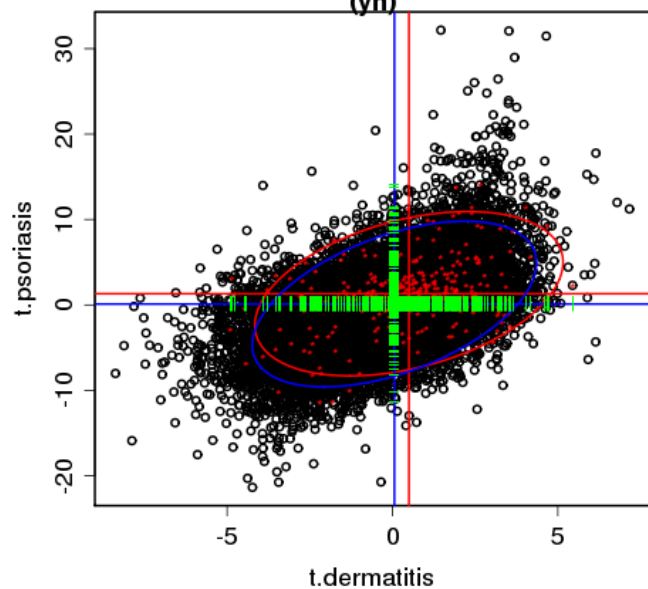
GO:0009889
regulation of biosynthetic process
(yh)



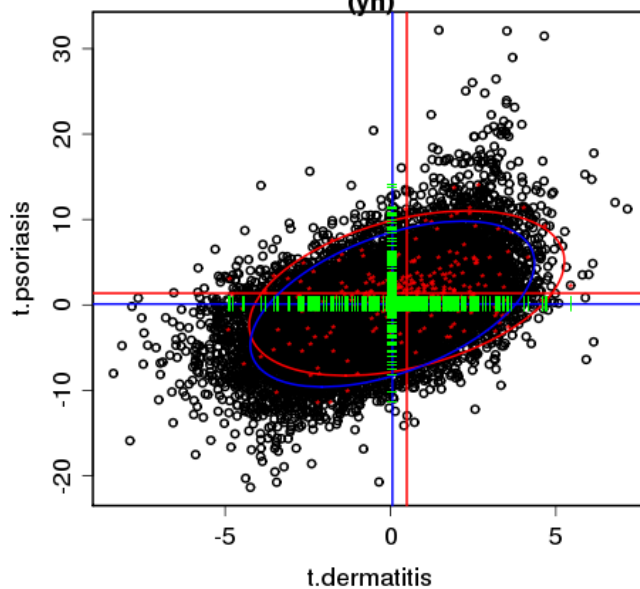
GO:0031326
regulation of cellular biosynthetic process
(yh)



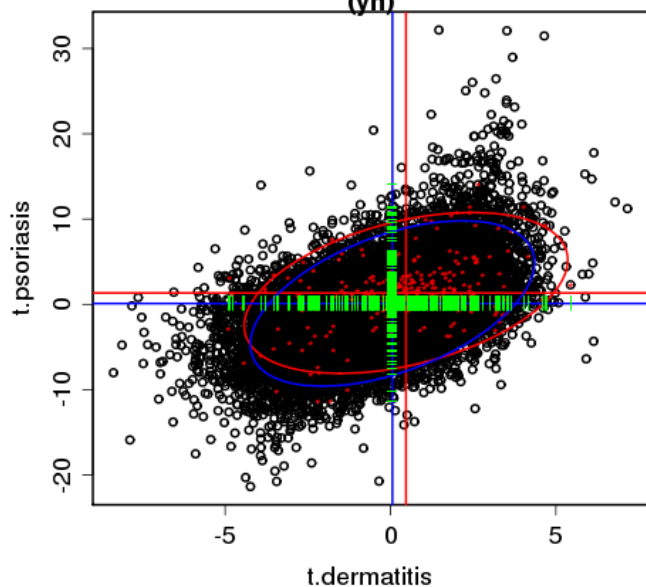
GO:0001775
cell activation
(yh)



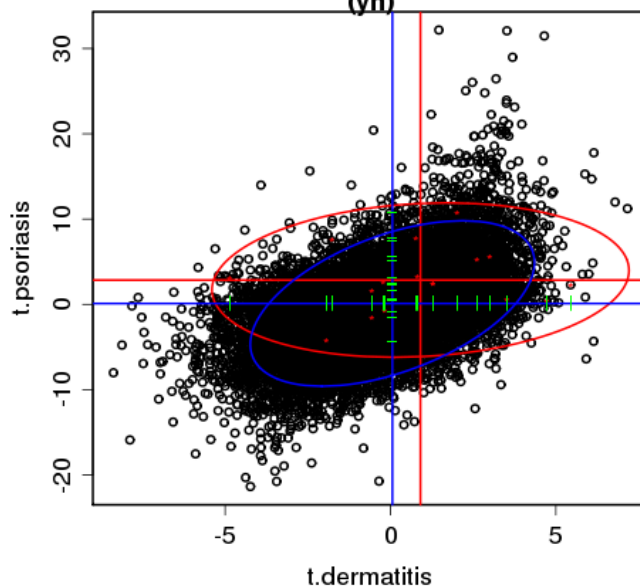
GO:0045321
leukocyte activation
(yh)



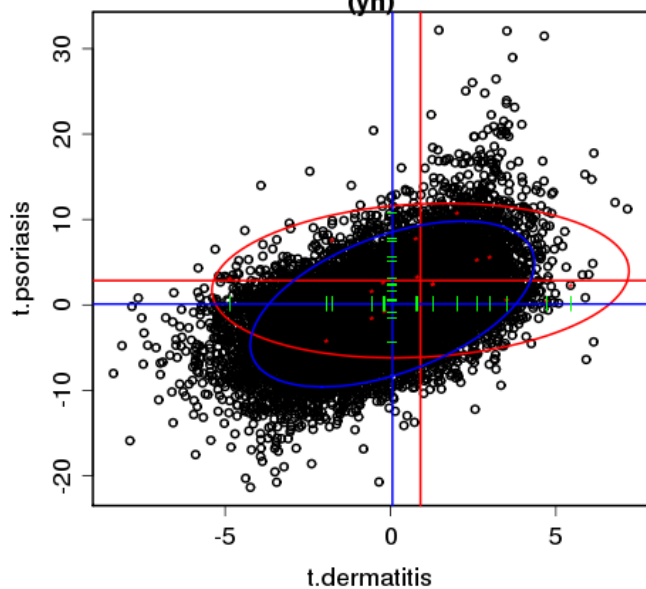
GO:0046649
lymphocyte activation
(yh)



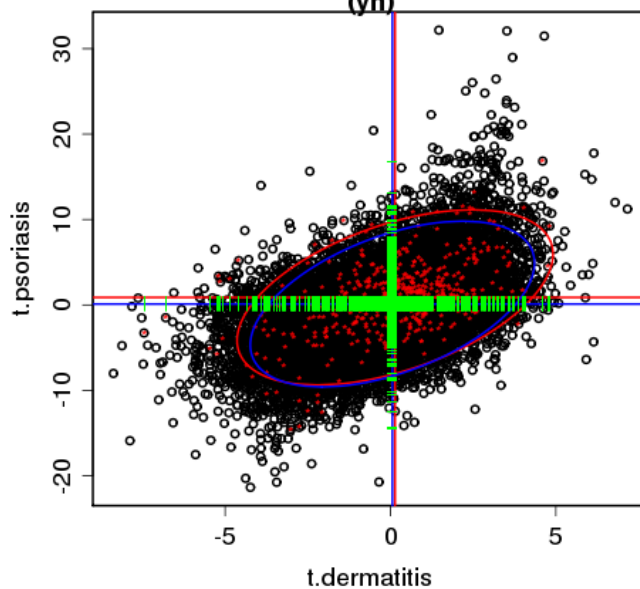
GO:0050854
regulation of antigen receptor-mediated signaling pathw
(yh)



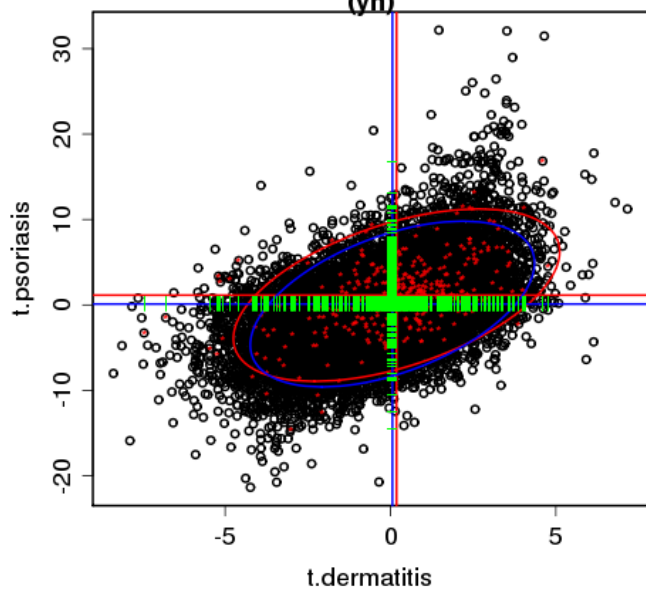
GO:0050856
regulation of T cell receptor signaling pathway
(yh)



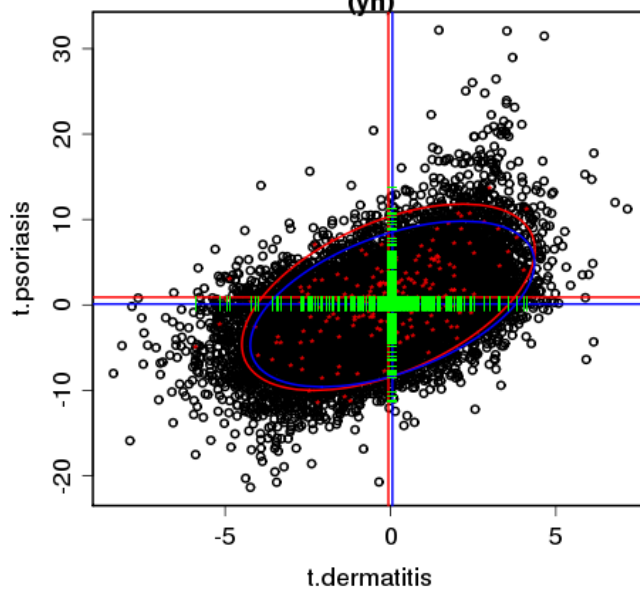
GO:0051094
positive regulation of developmental process
(yh)

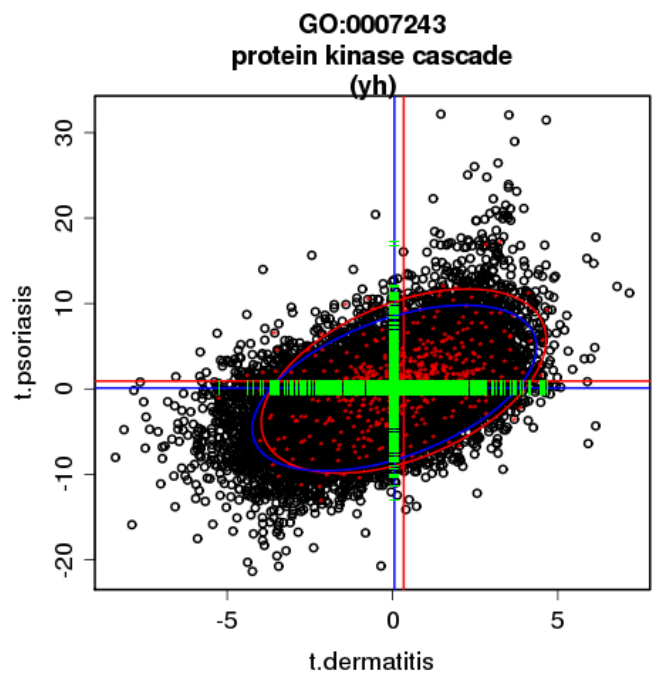
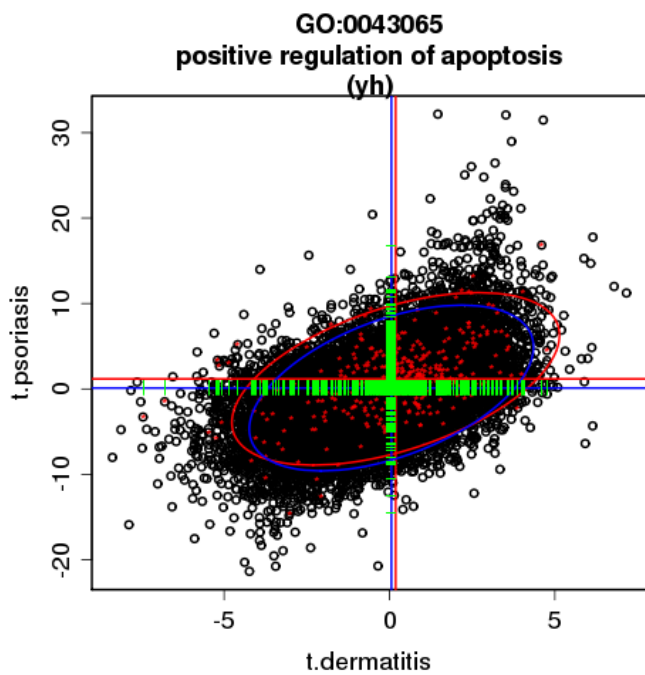
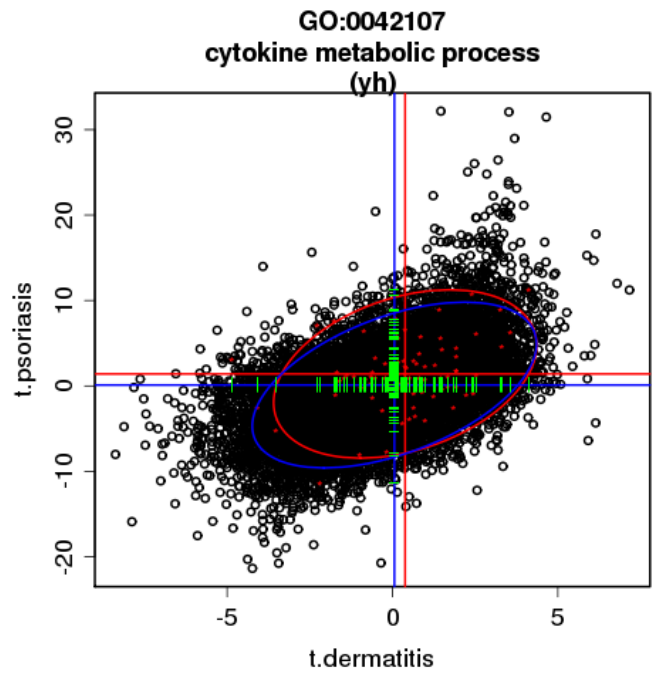
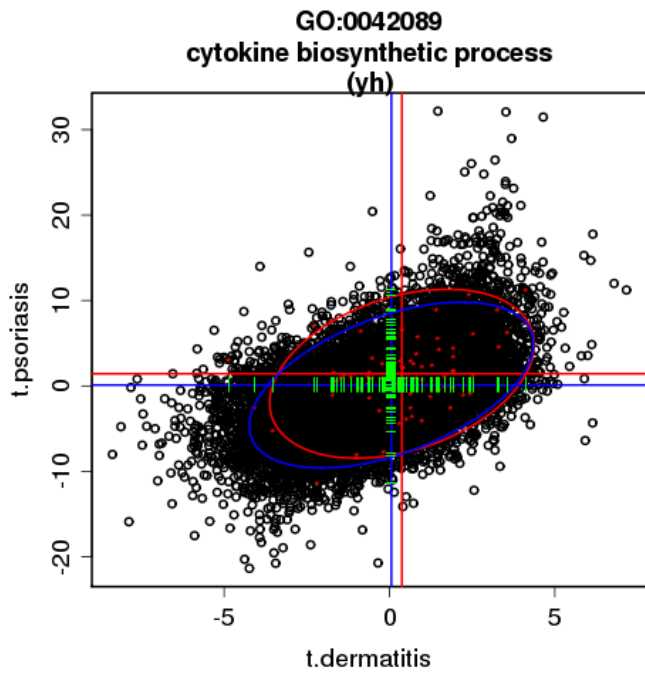
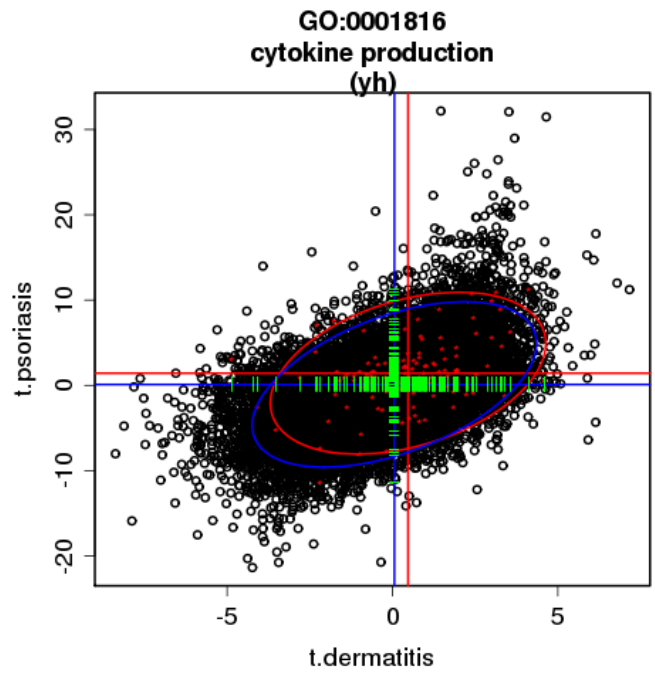
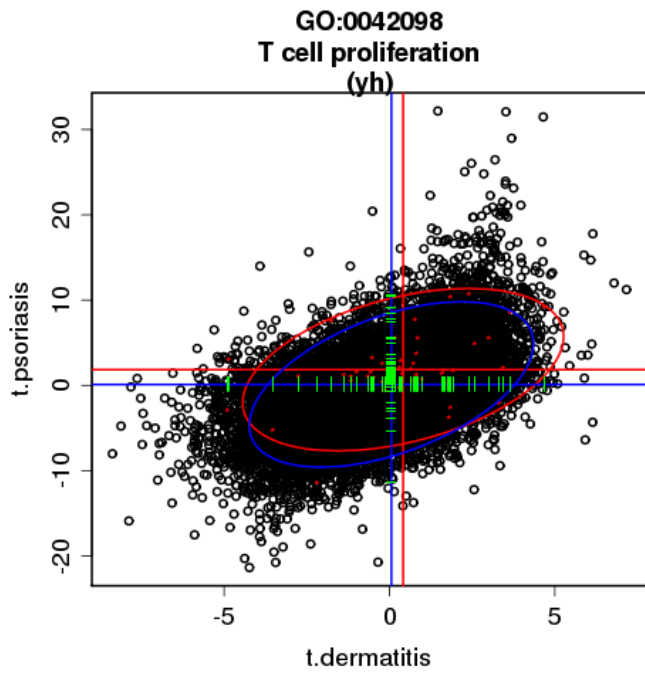


GO:0043068
positive regulation of programmed cell death
(yh)

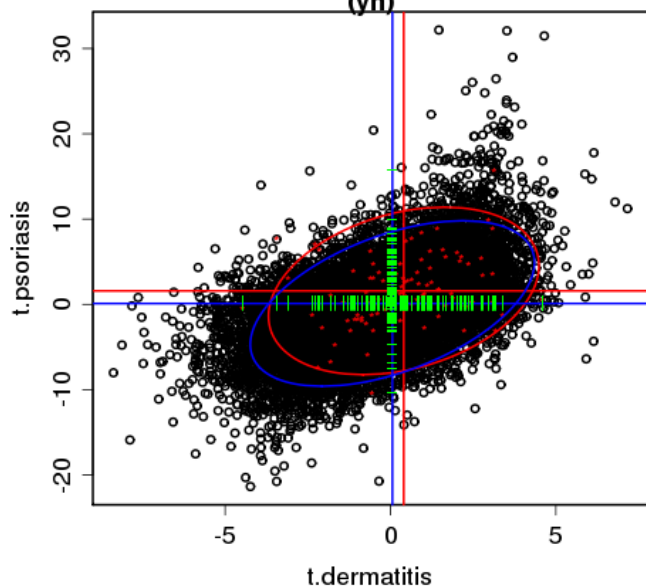


GO:0006417
regulation of translation
(yh)

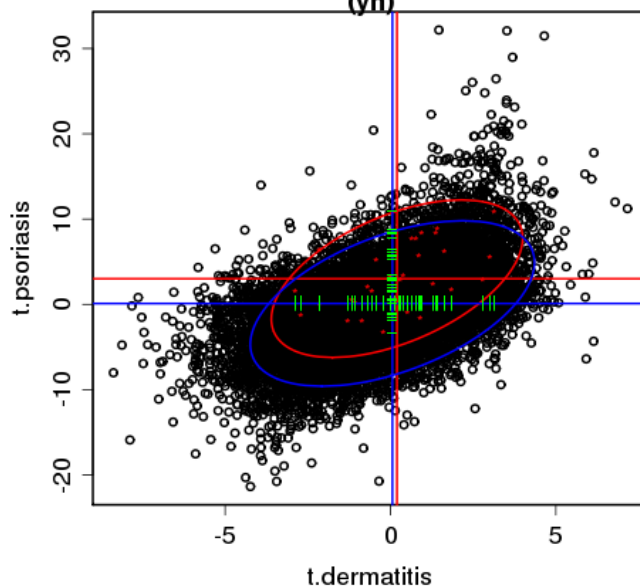




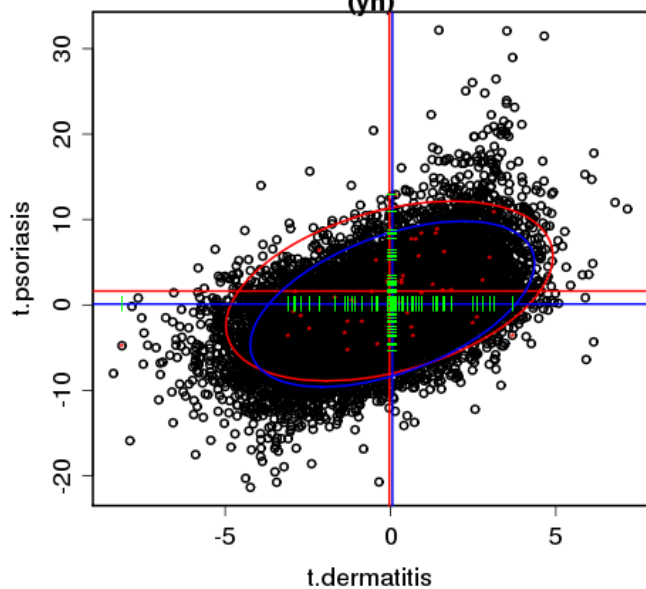
GO:0051052
regulation of DNA metabolic process
(yh)



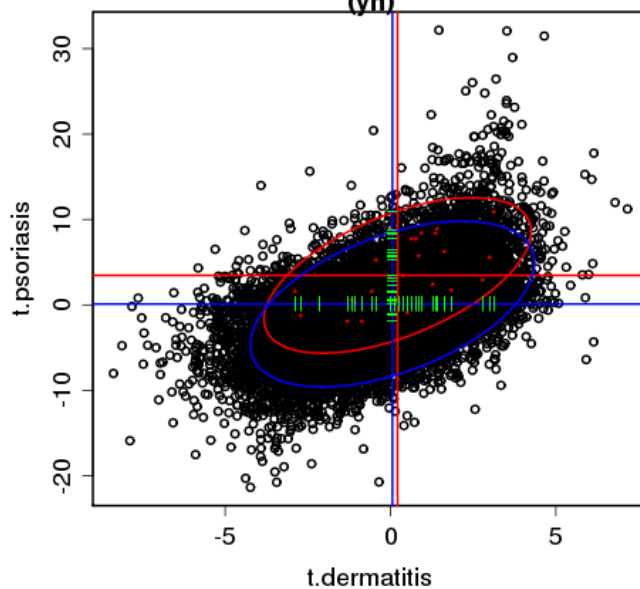
GO:0043388
positive regulation of DNA binding
(yh)



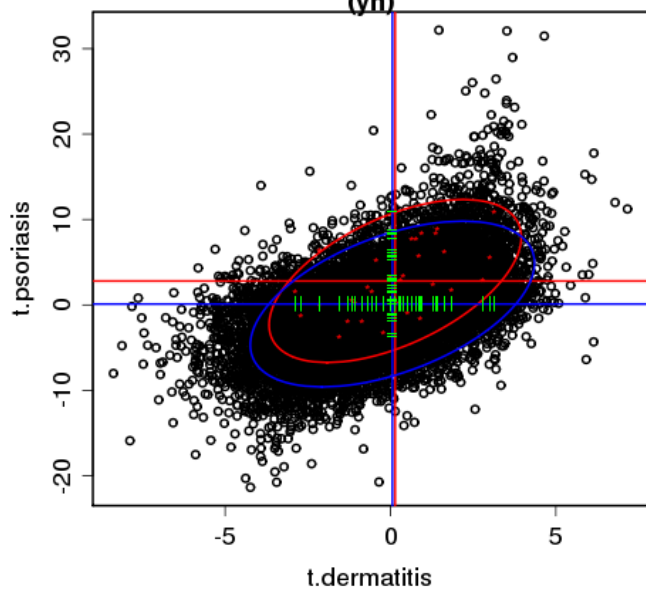
GO:0051090
regulation of transcription factor activity
(yh)



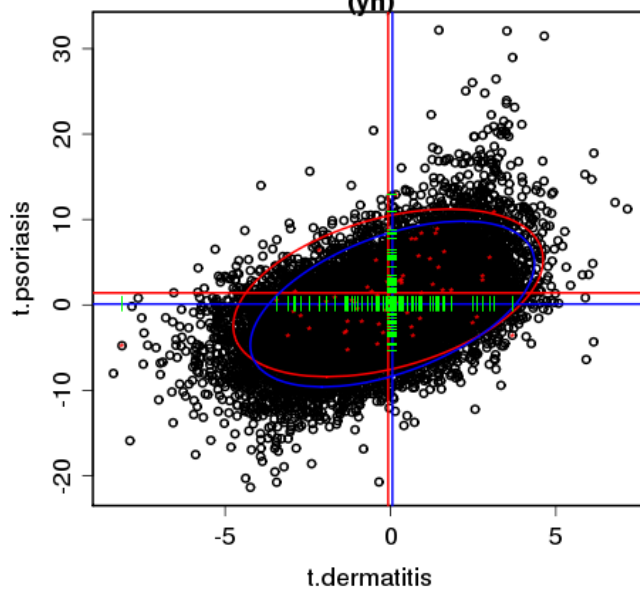
GO:0051091
positive regulation of transcription factor activity
(yh)



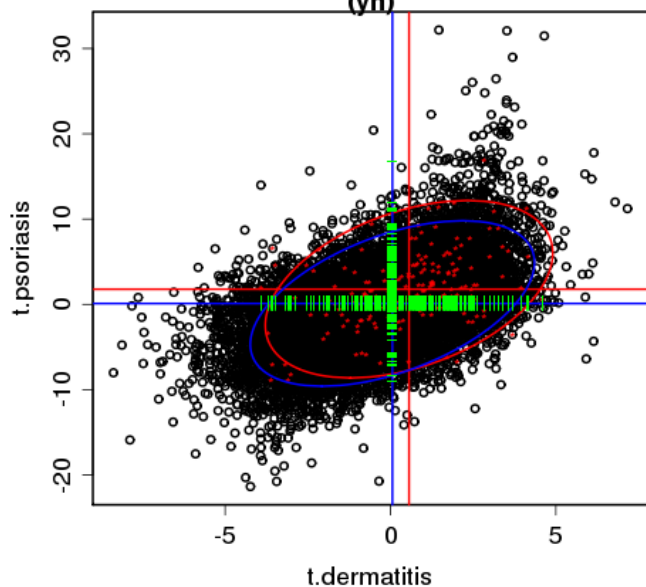
GO:0051099
positive regulation of binding
(yh)



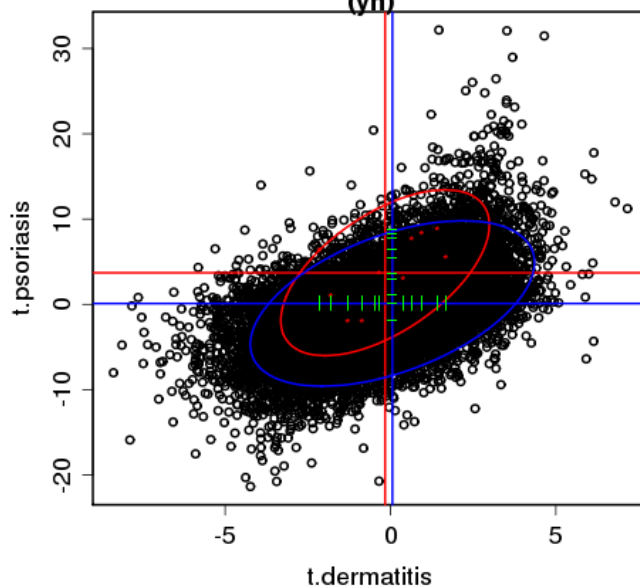
GO:0051101
regulation of DNA binding
(yh)



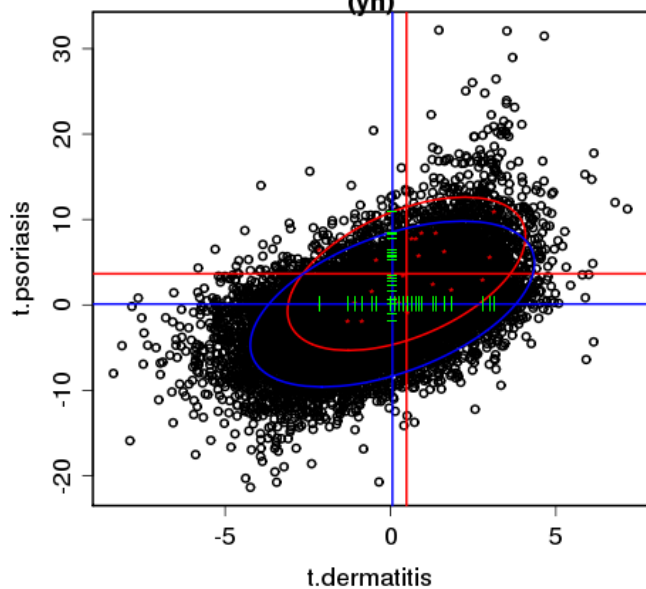
GO:0007249
I-kappaB kinase/NF-kappaB cascade
(yh)



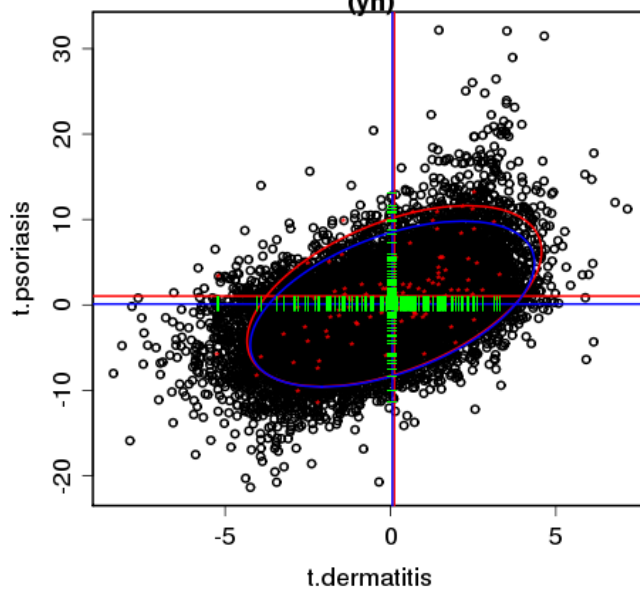
GO:0006282
regulation of DNA repair
(yh)



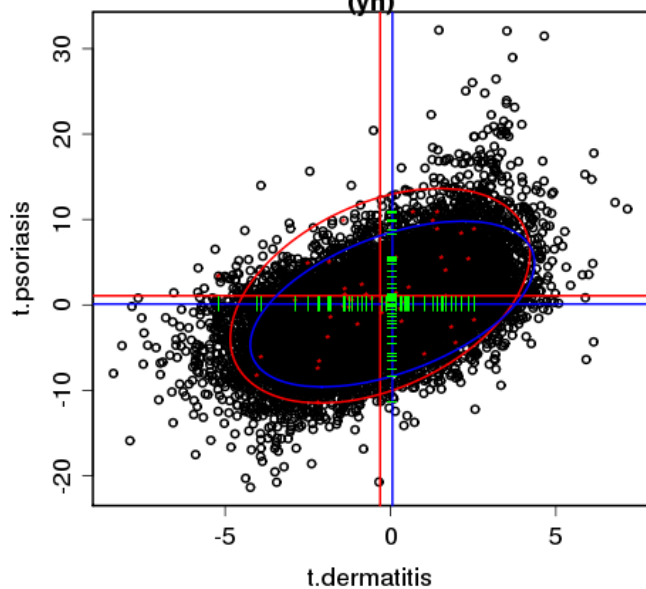
GO:0051092
positive regulation of NF-kappaB transcription factor acti
(yh)



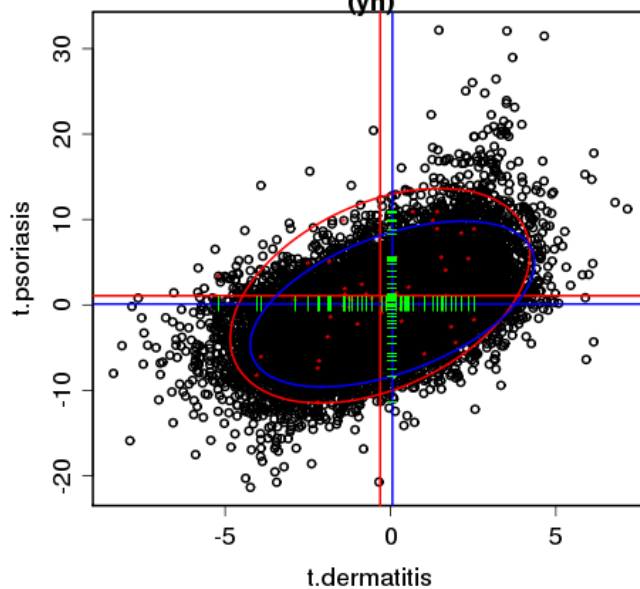
GO:0030099
myeloid cell differentiation
(yh)

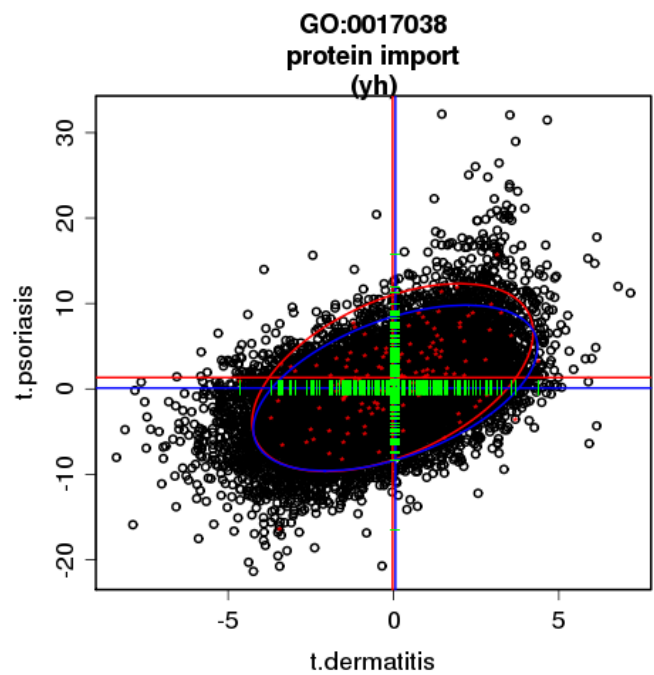
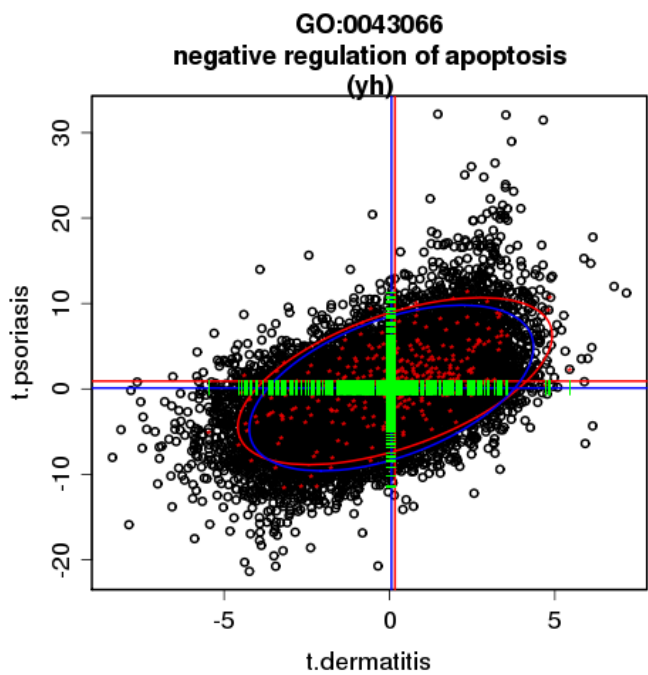
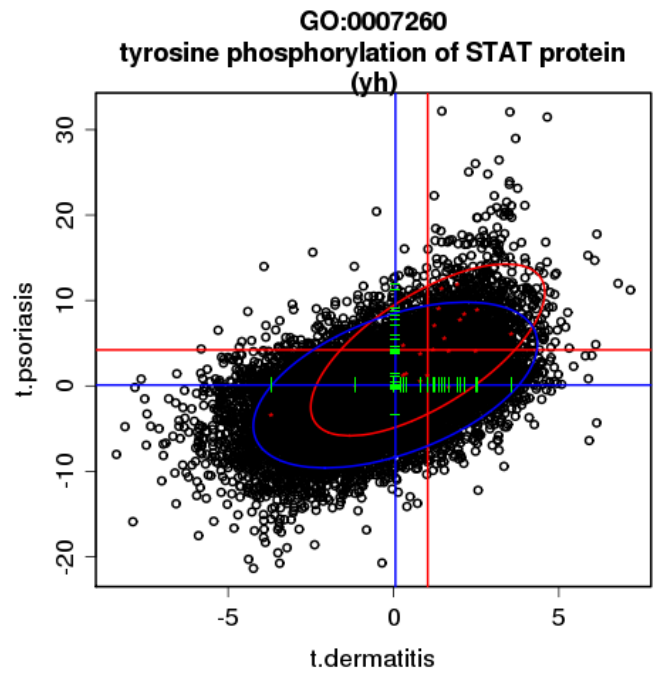
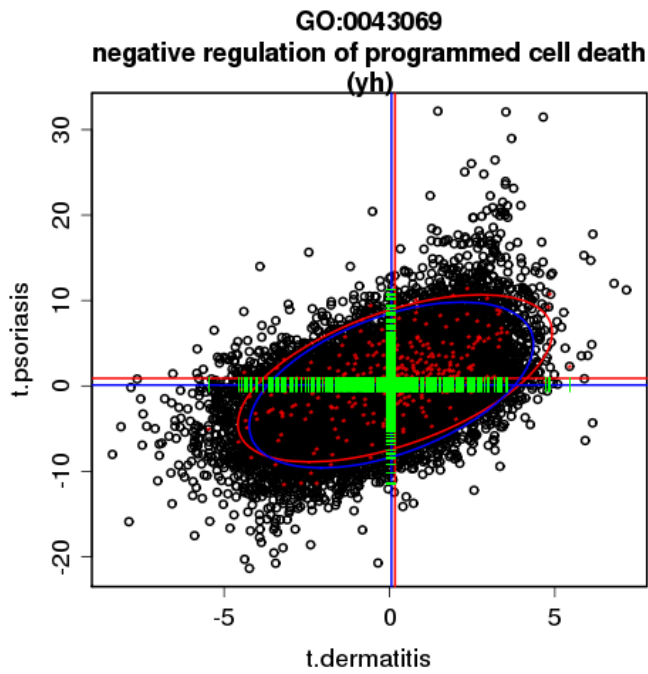
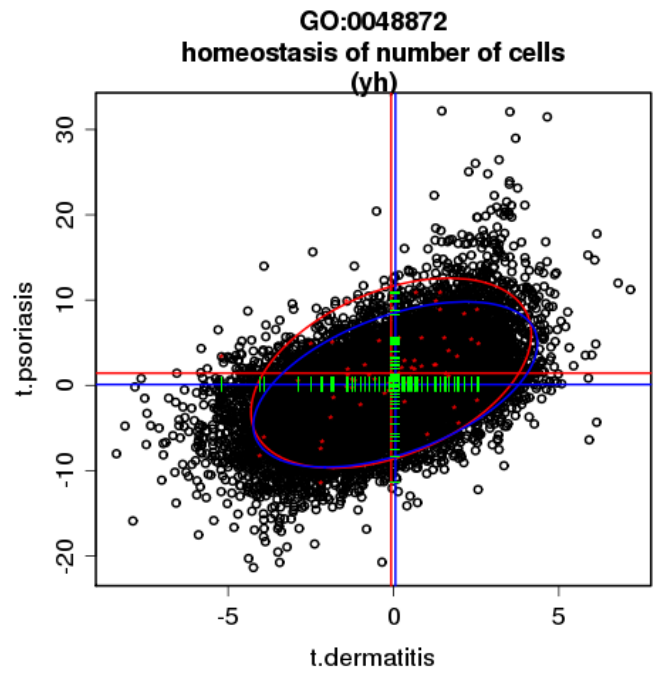
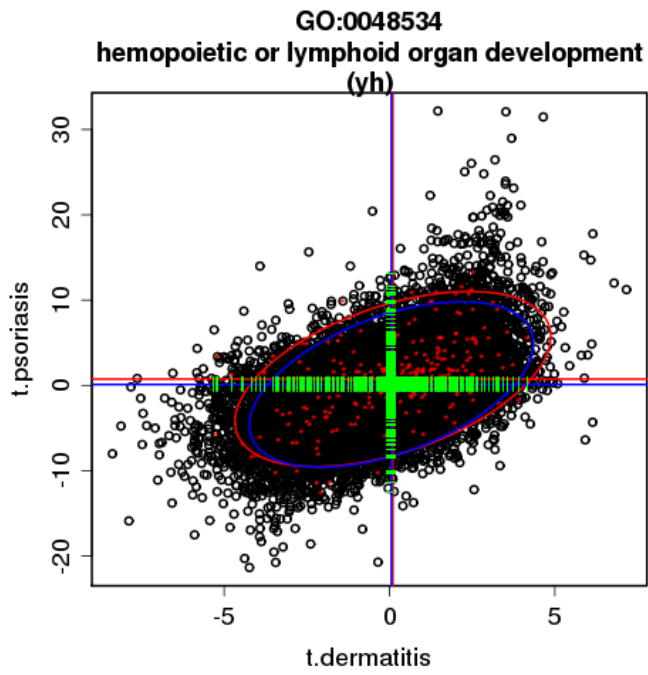


GO:0030218
erythrocyte differentiation
(yh)

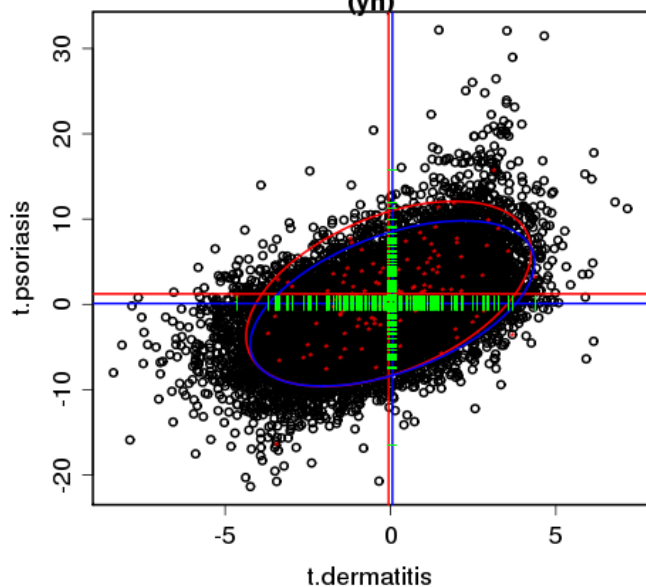


GO:0034101
erythrocyte homeostasis
(yh)

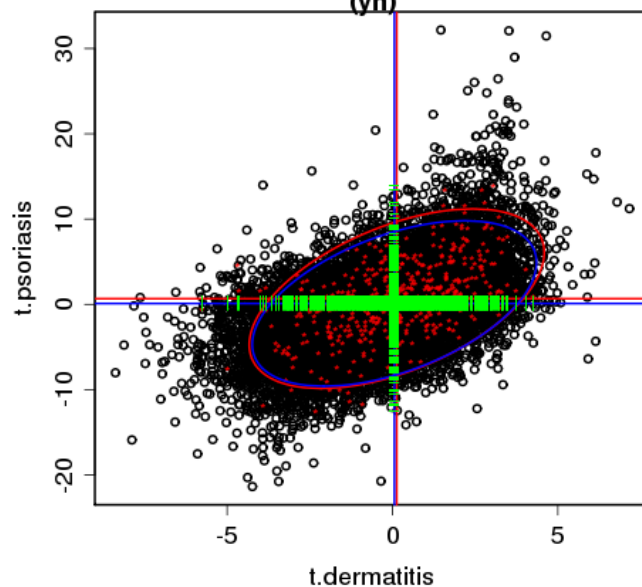




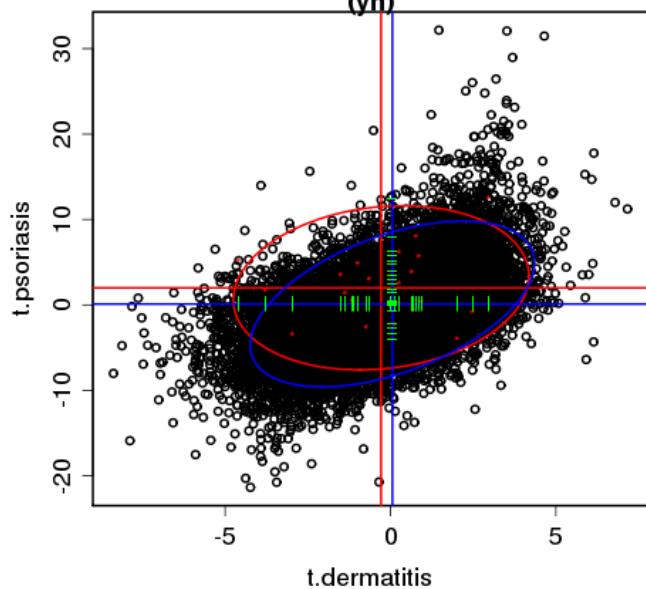
GO:0051170
nuclear import
(yh)



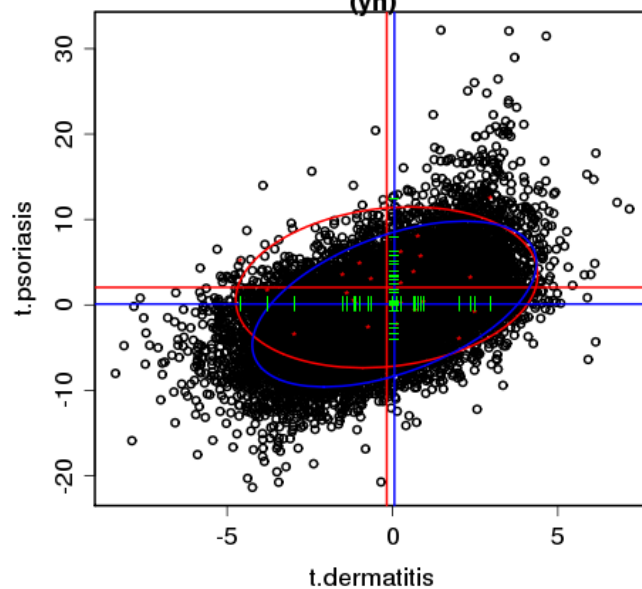
GO:0009057
macromolecule catabolic process
(yh)



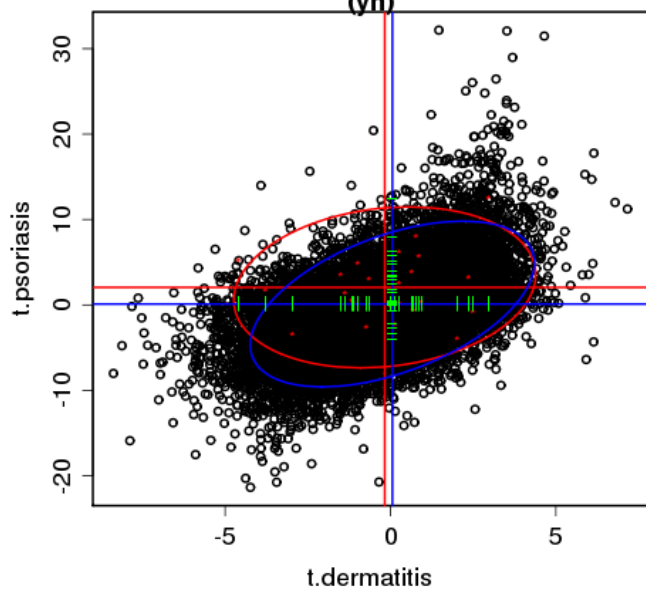
GO:0022404
molting cycle process
(yh)



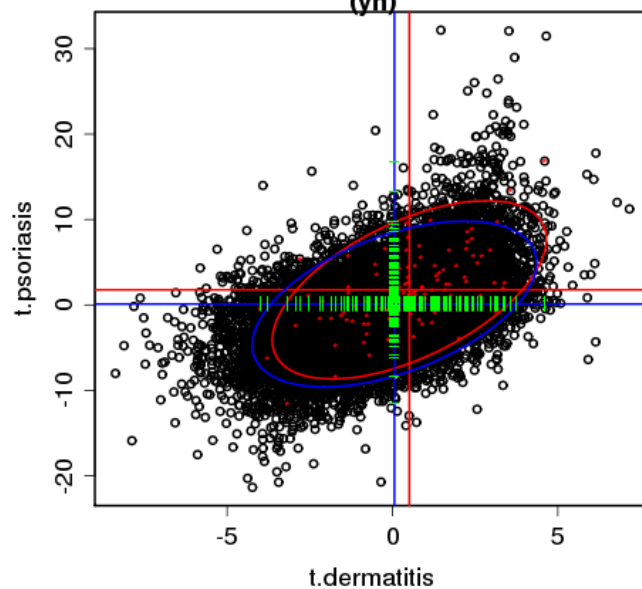
GO:0042303
molting cycle
(yh)

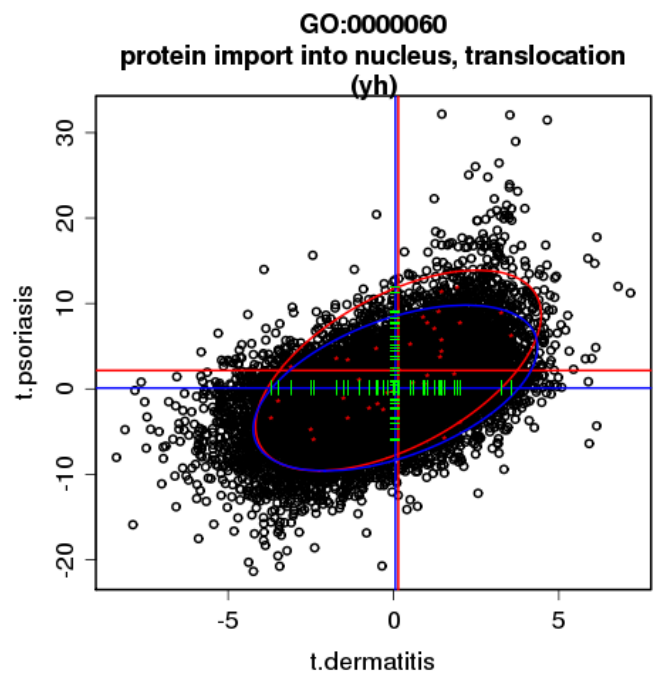
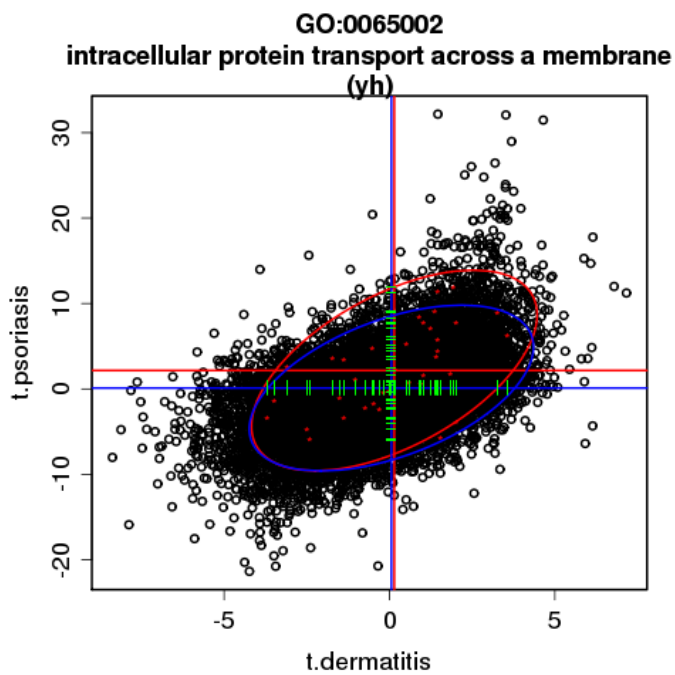
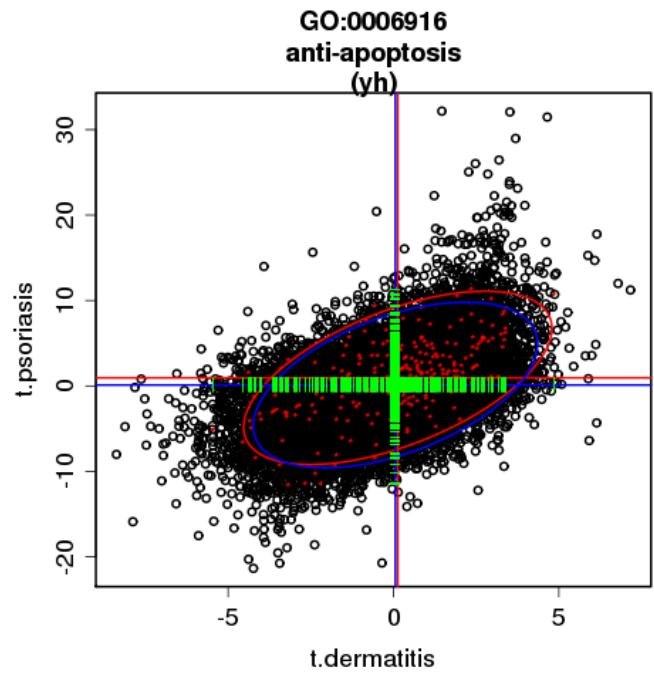
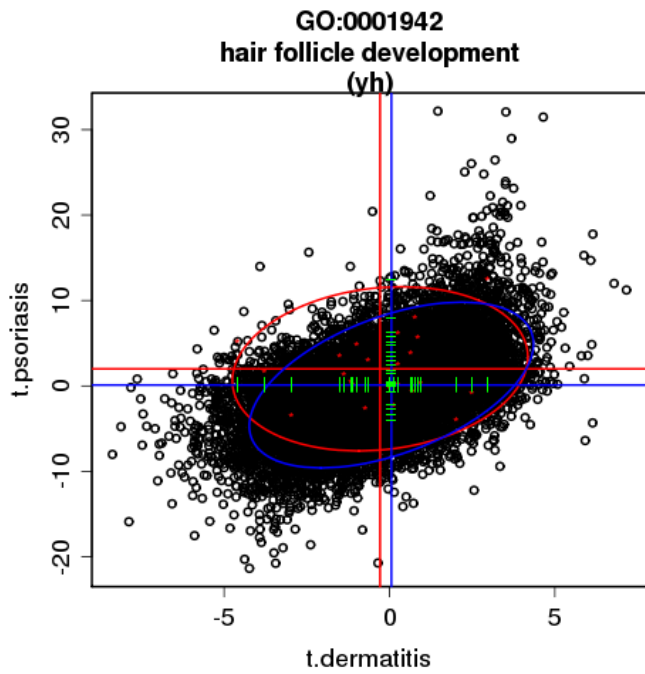
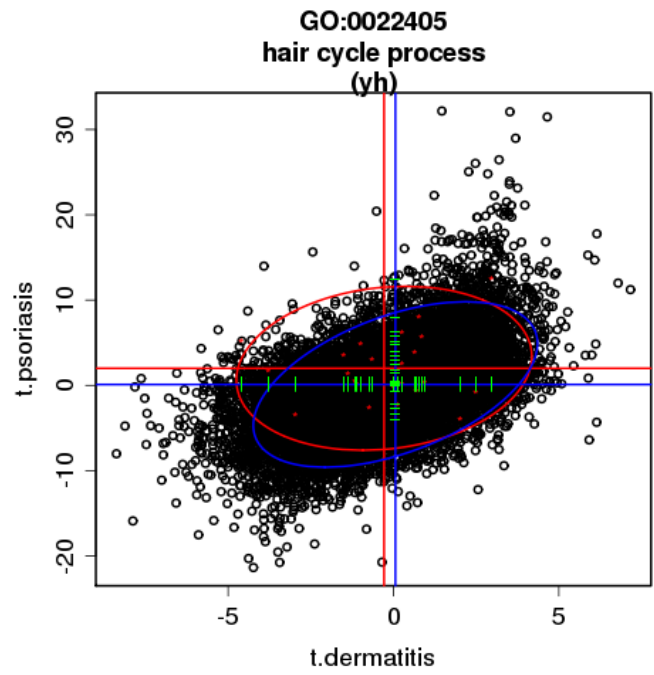
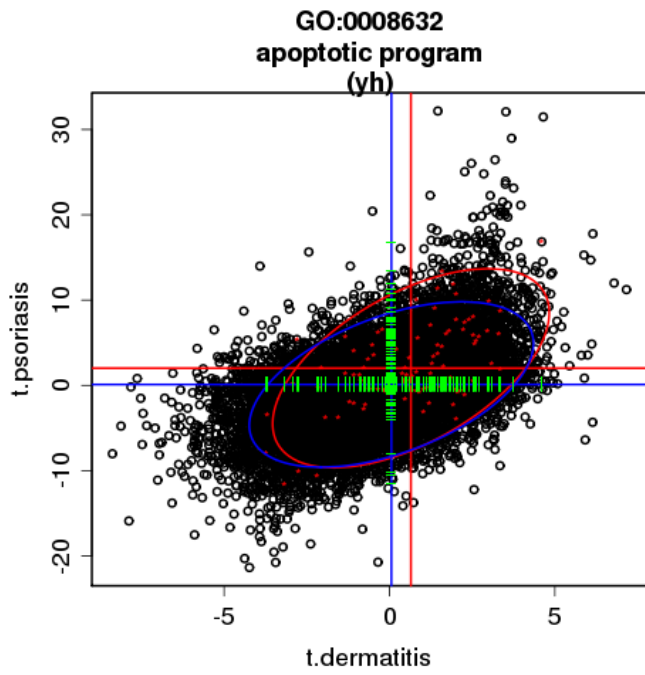


GO:0042633
hair cycle
(yh)

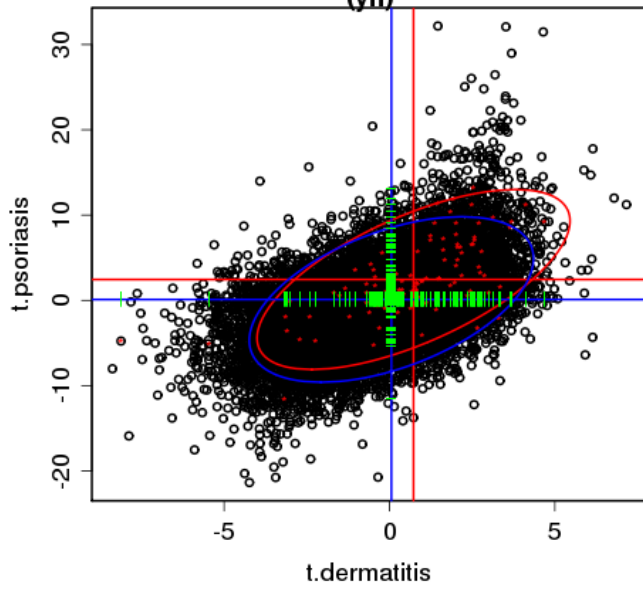


GO:0007005
mitochondrion organization and biogenesis
(yh)

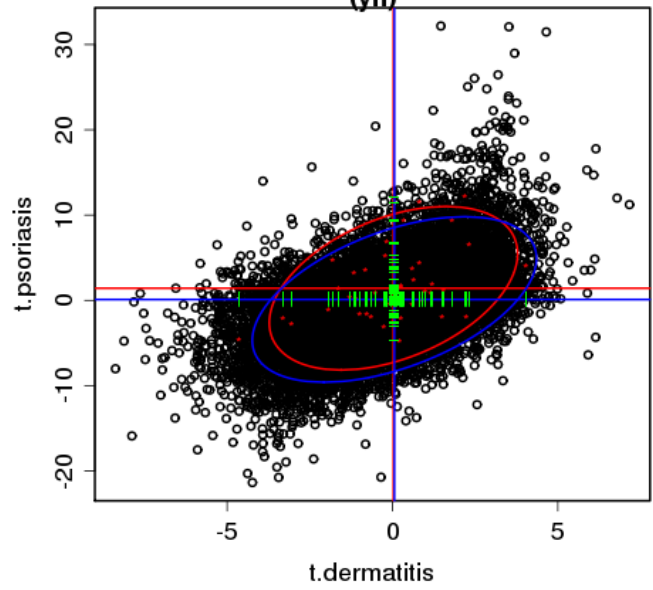




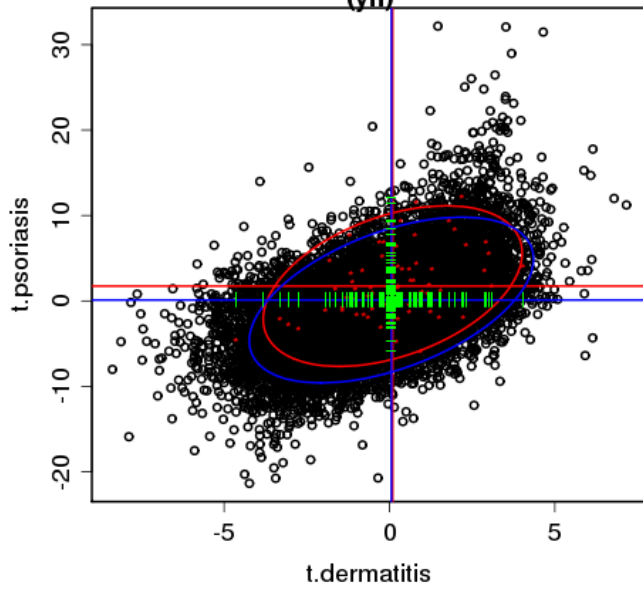
GO:0009615
response to virus
(yh)



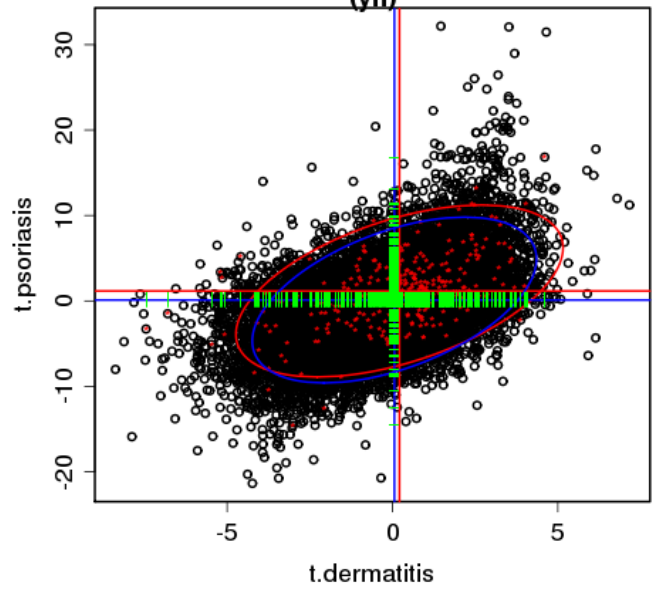
GO:0006405
RNA export from nucleus
(yh)



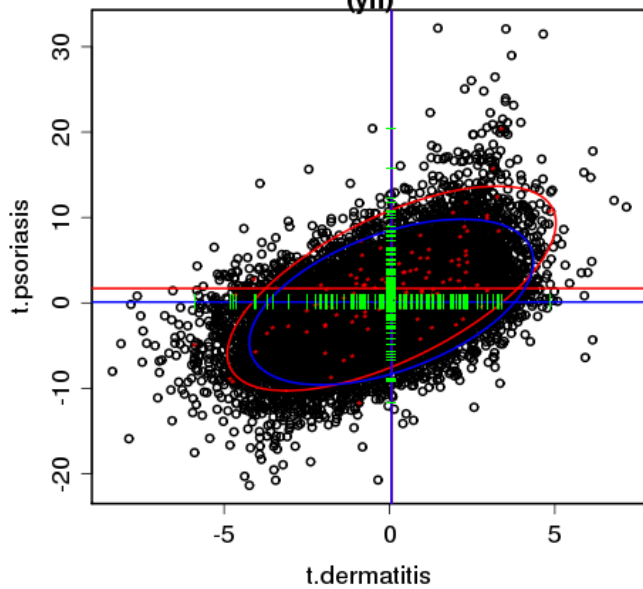
GO:0051168
nuclear export
(yh)



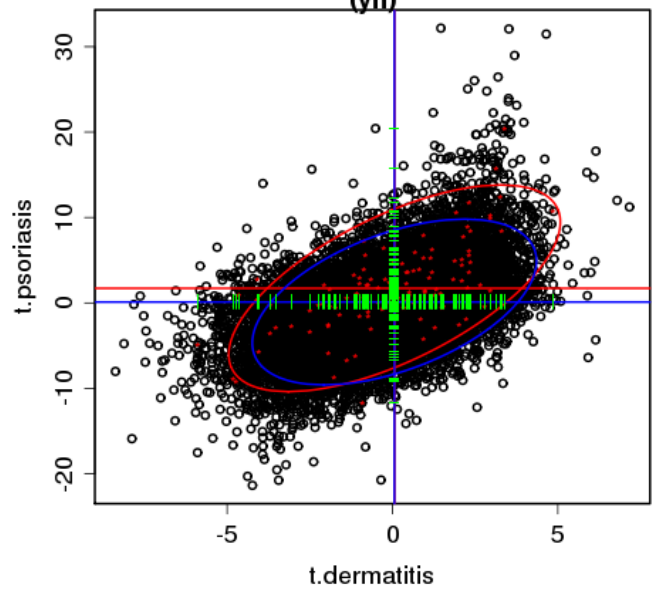
GO:0012502
induction of programmed cell death
(yh)

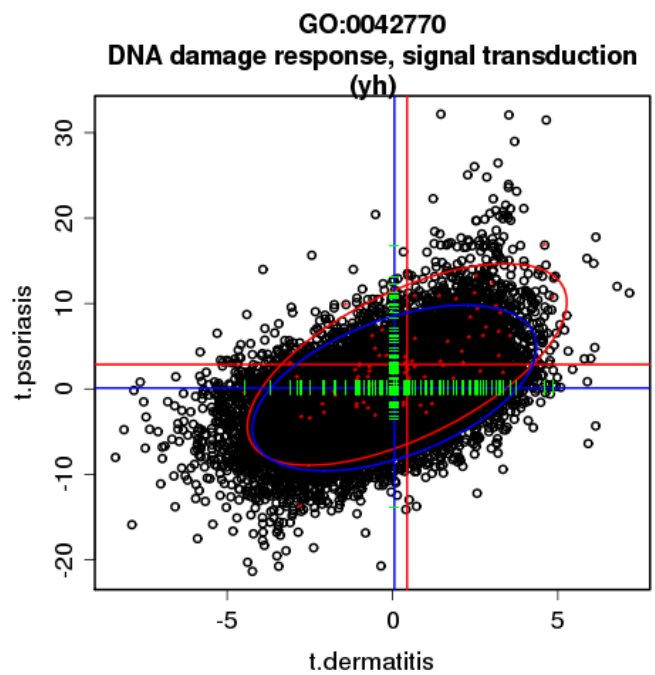
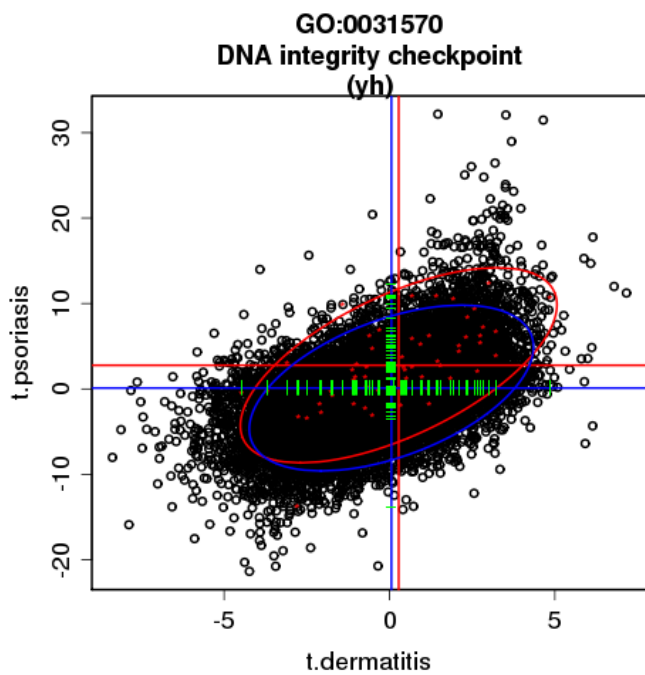
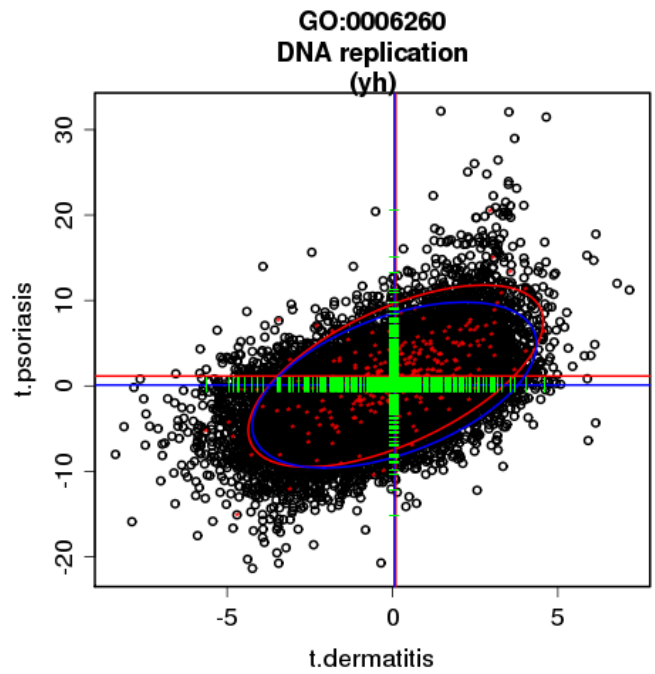
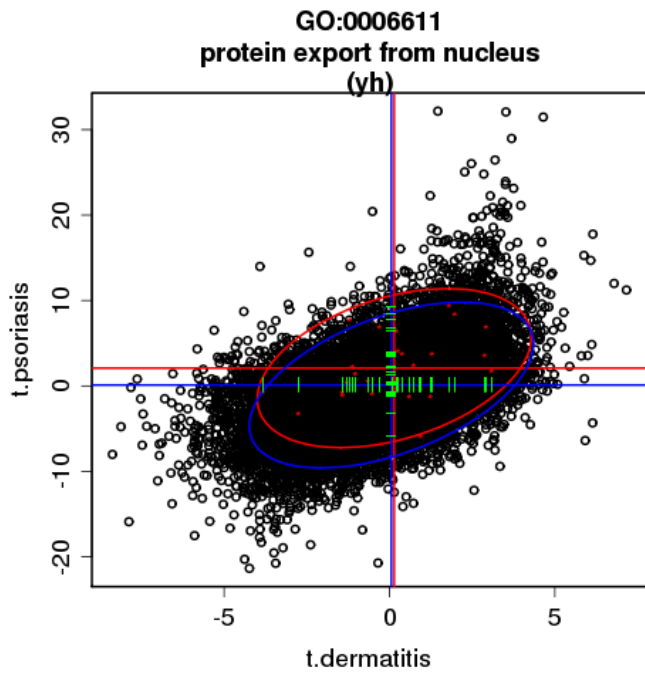
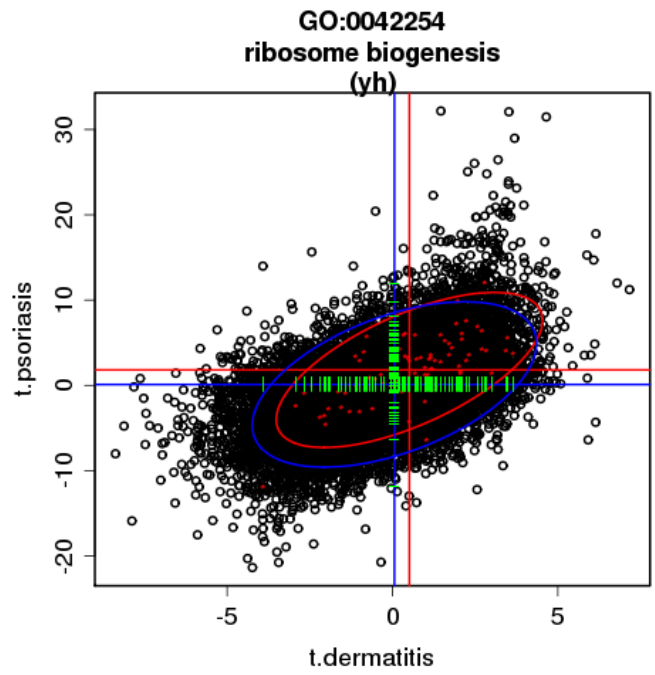
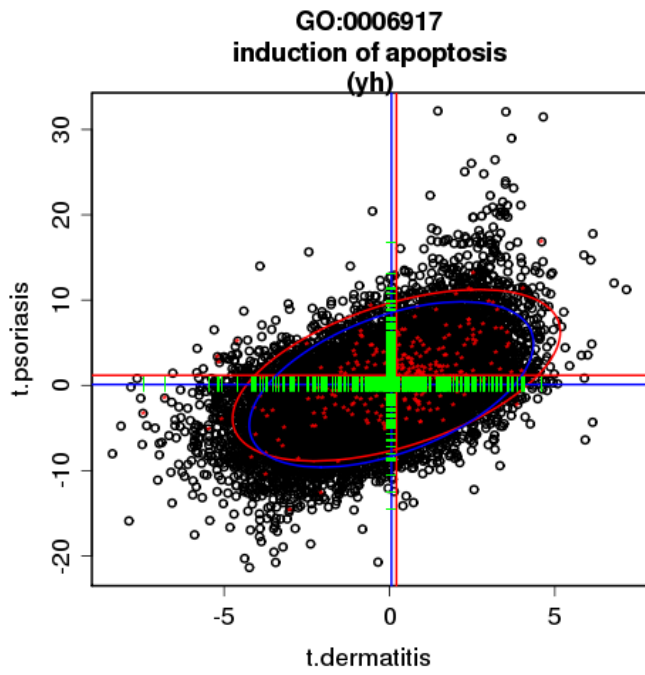


GO:0051325
interphase
(yh)

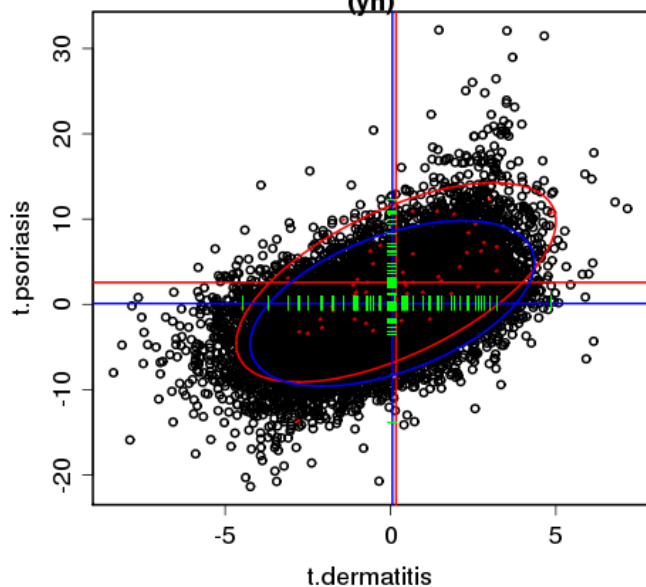


GO:0051329
interphase of mitotic cell cycle
(yh)

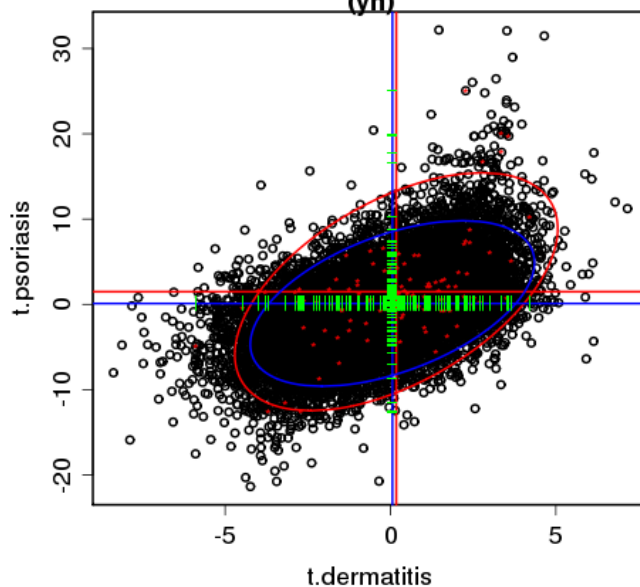




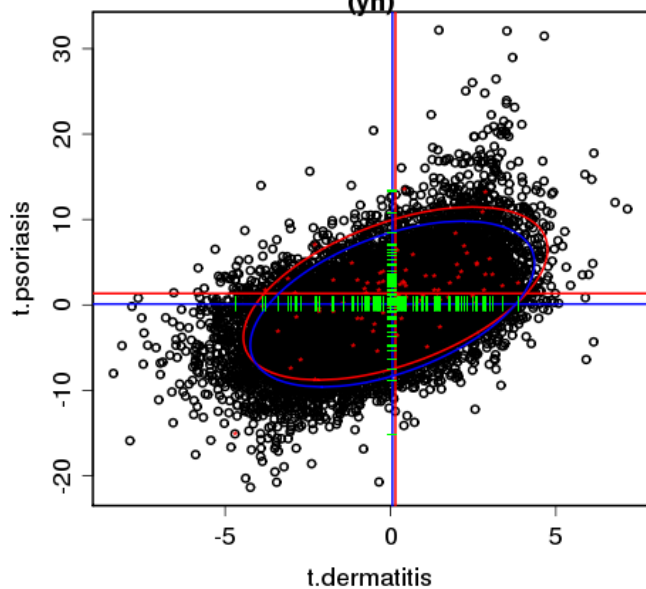
GO:0000077
DNA damage checkpoint
(yh)



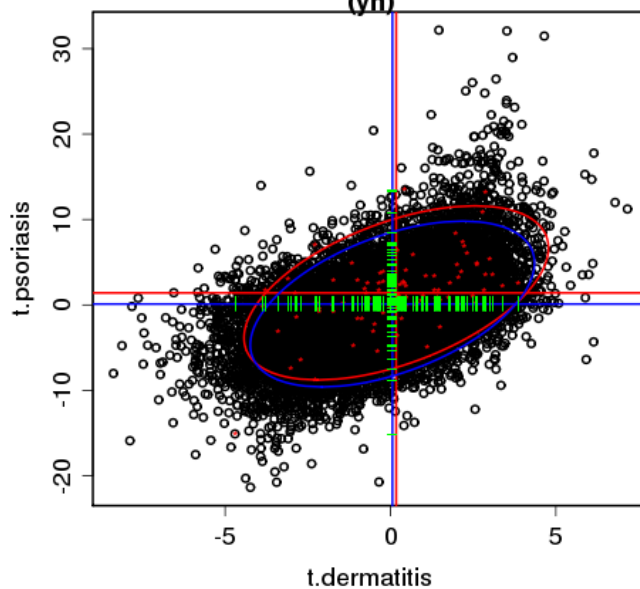
GO:0009314
response to radiation
(yh)



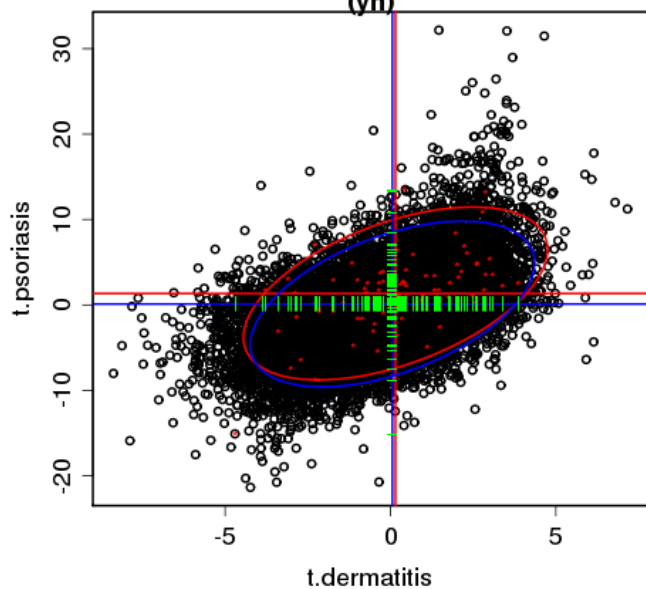
GO:0007126
meiosis
(yh)



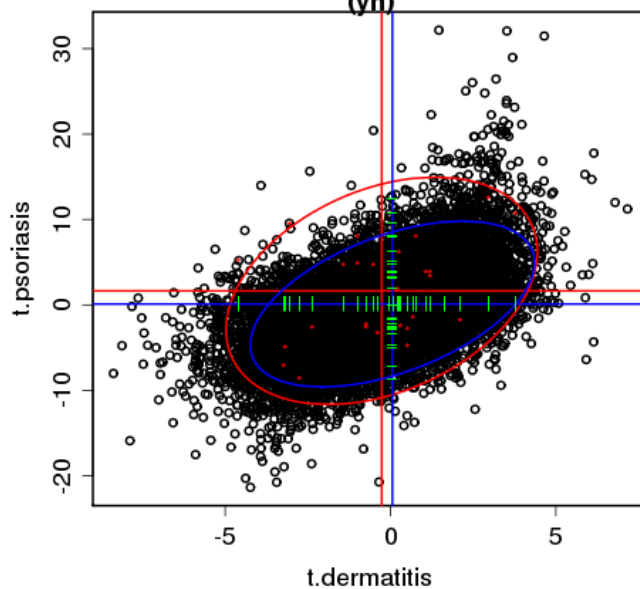
GO:0051321
meiotic cell cycle
(yh)



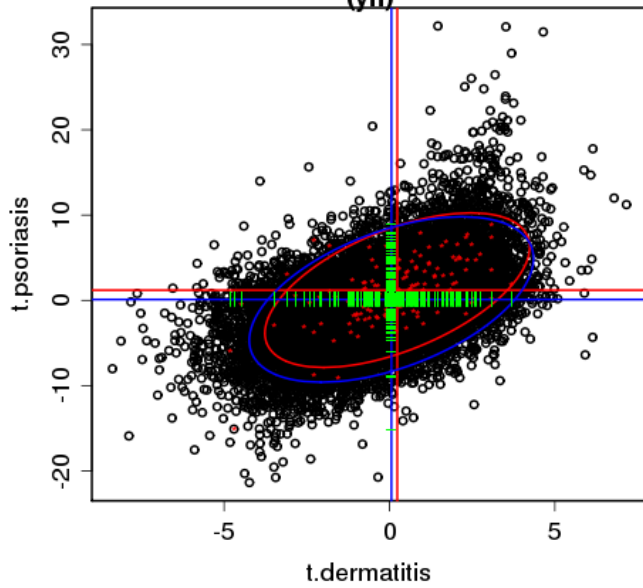
GO:0051327
M phase of meiotic cell cycle
(yh)



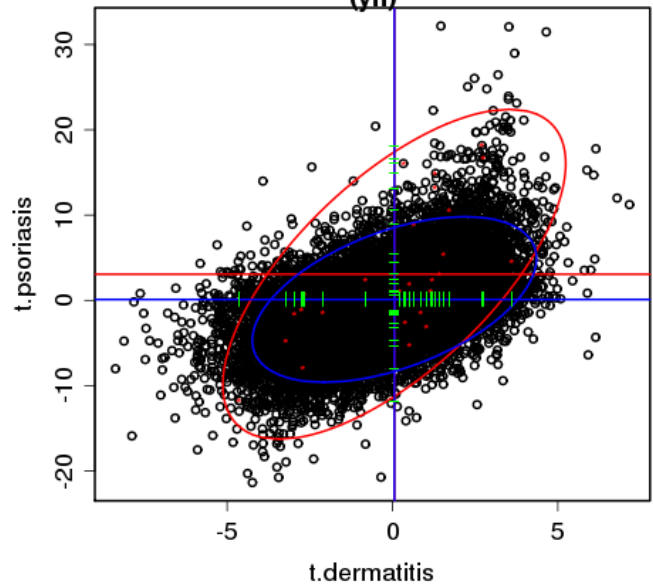
GO:0051262
protein tetramerization
(yh)



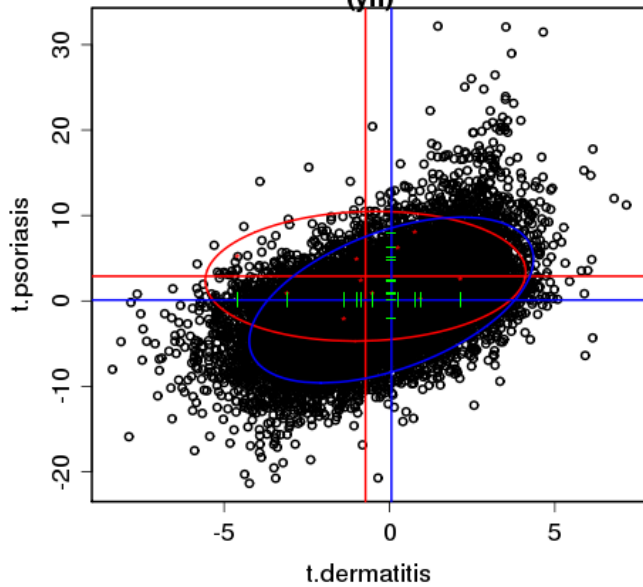
GO:0006261
DNA-dependent DNA replication
(yh)



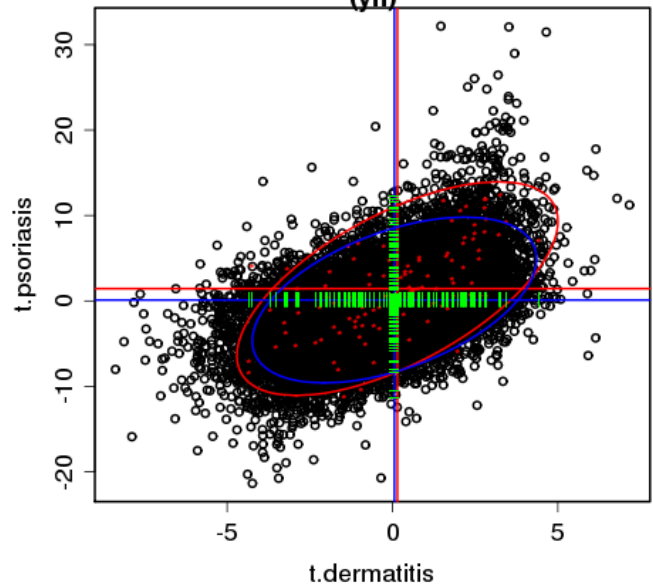
GO:0046466
membrane lipid catabolic process
(yh)



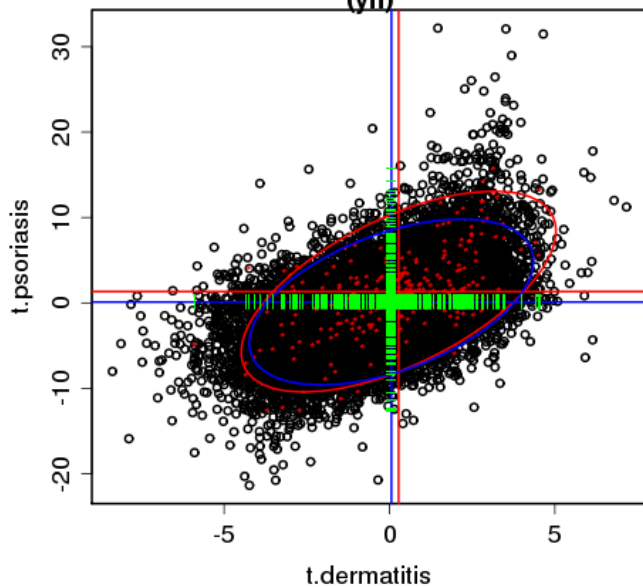
GO:0007164
establishment of tissue polarity
(yh)



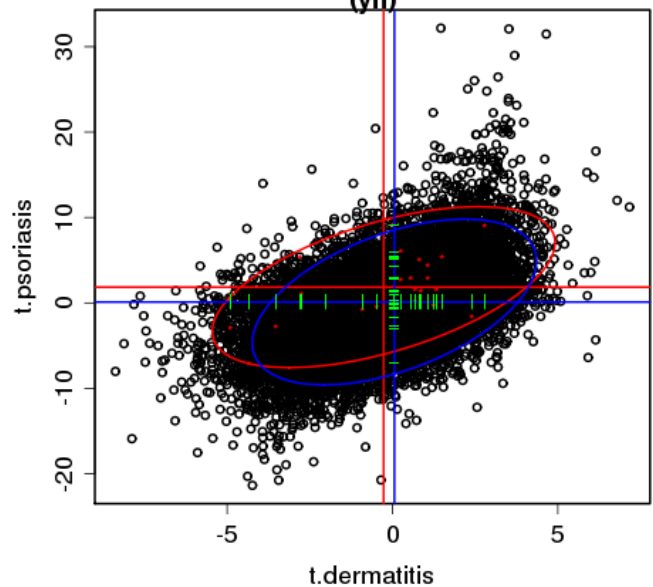
GO:0000226
microtubule cytoskeleton organization and biogenesis
(yh)



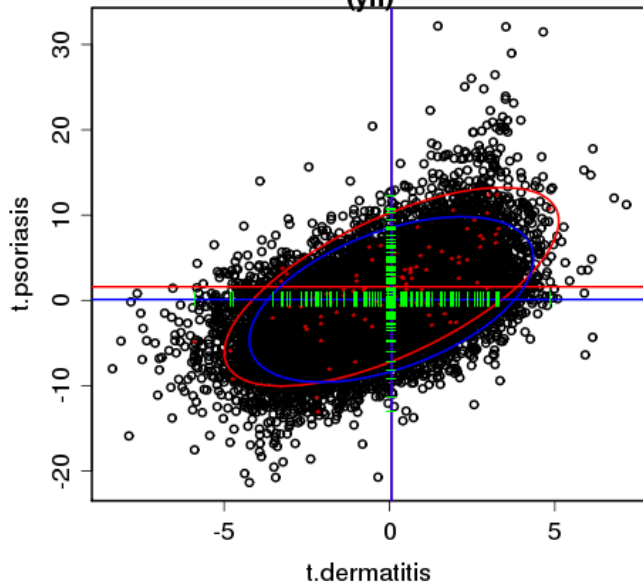
GO:0007017
microtubule-based process
(yh)



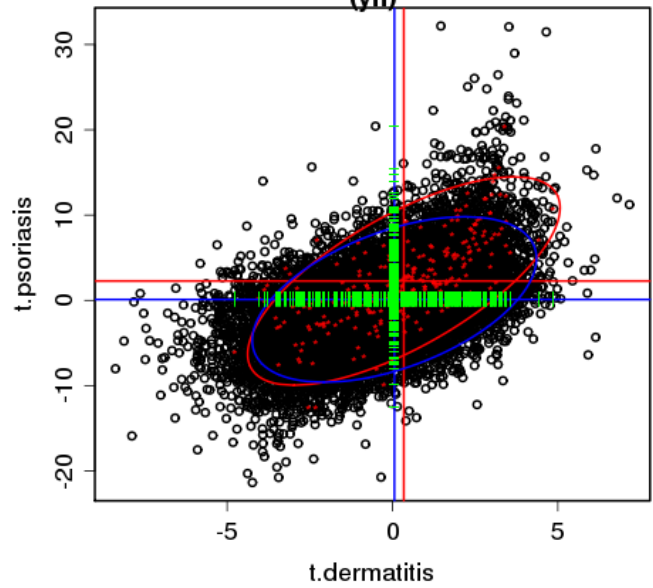
GO:0032271
regulation of protein polymerization
(yh)



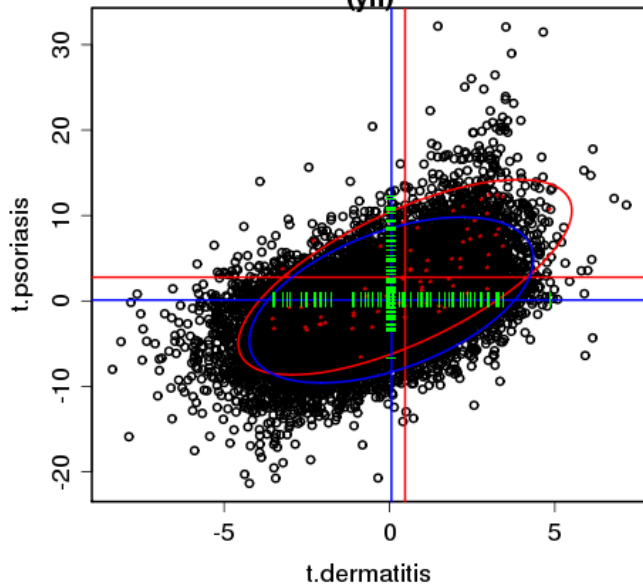
GO:0007346
regulation of mitotic cell cycle
(yh)



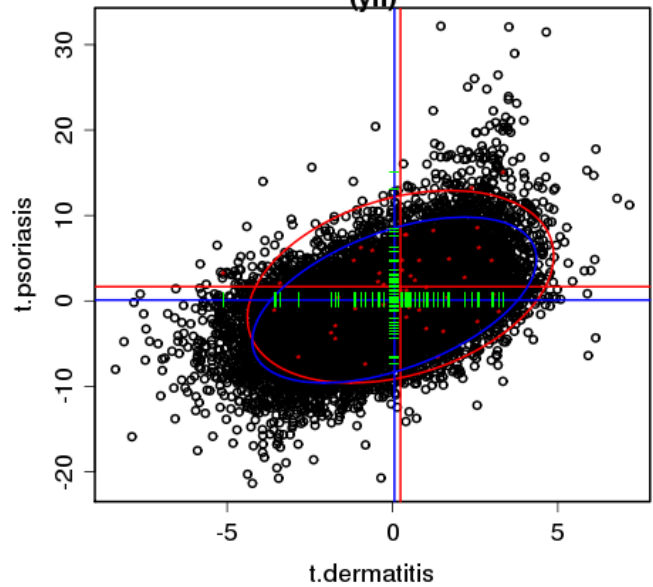
GO:0007067
mitosis
(yh)



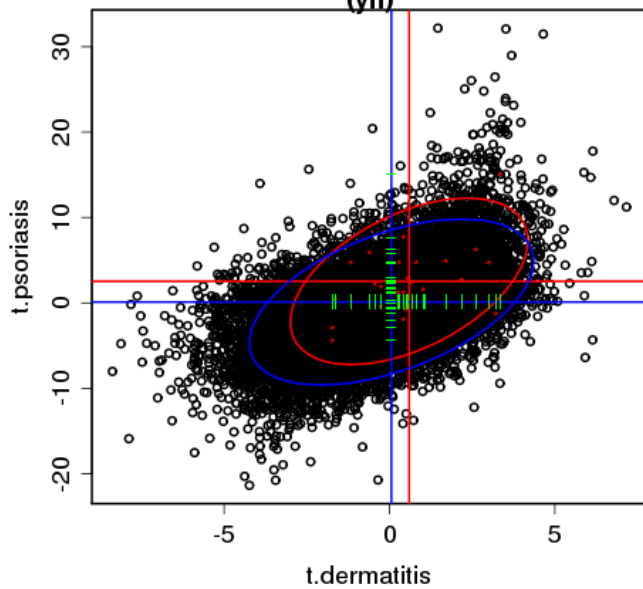
GO:0007088
regulation of mitosis
(yh)



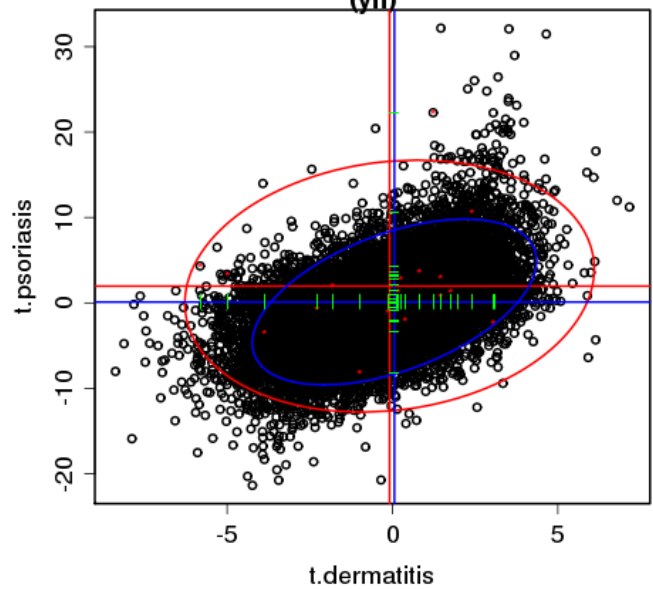
GO:0006767
water-soluble vitamin metabolic process
(yh)



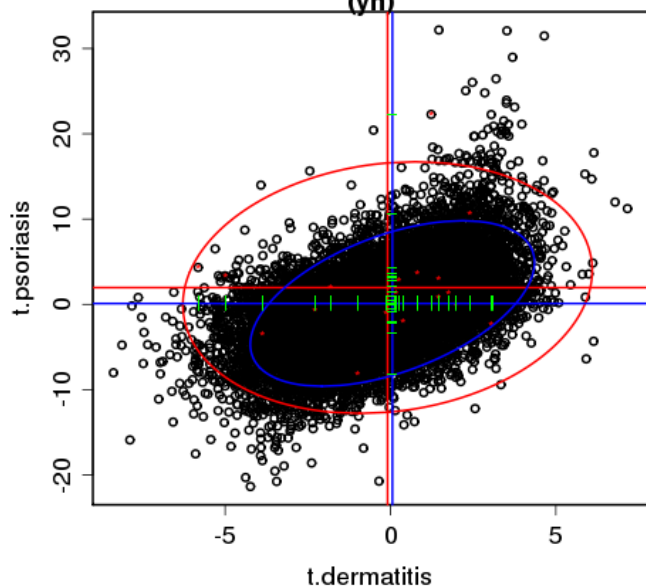
GO:0006769
nicotinamide metabolic process
(yh)



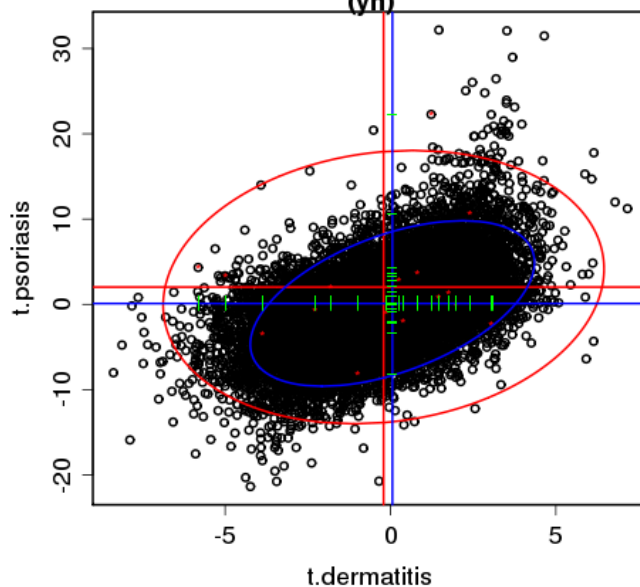
GO:0006691
leukotriene metabolic process
(yh)



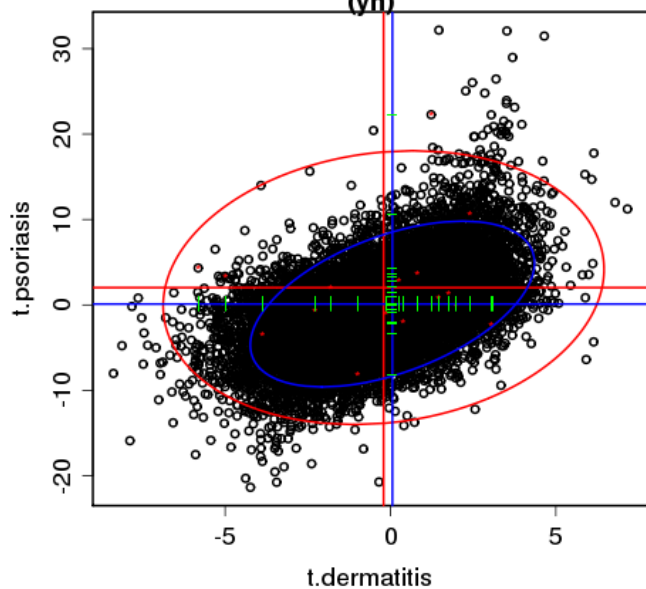
GO:0043449
alkene metabolic process
(yh)



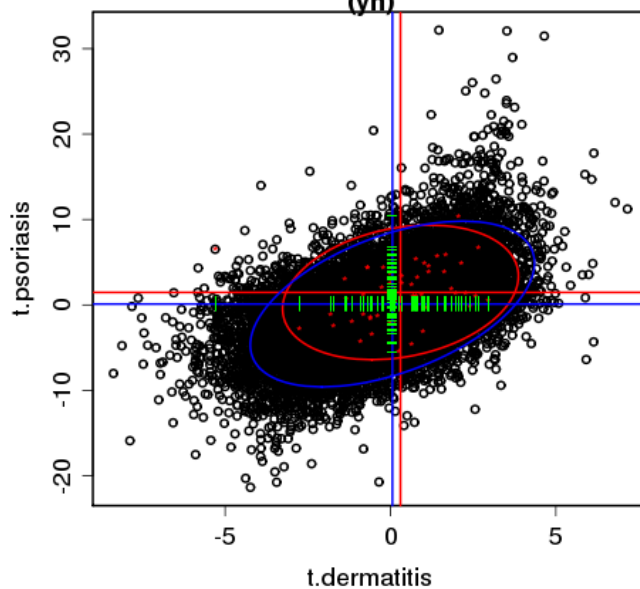
GO:0043450
alkene biosynthetic process
(yh)



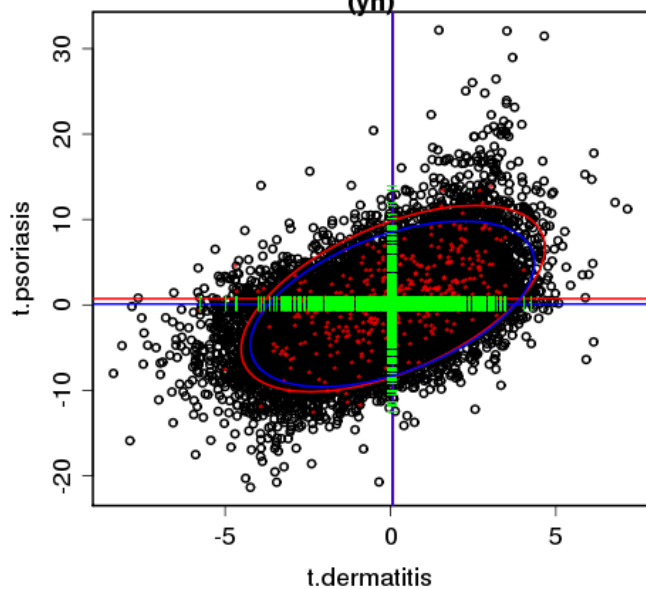
GO:0019370
leukotriene biosynthetic process
(yh)



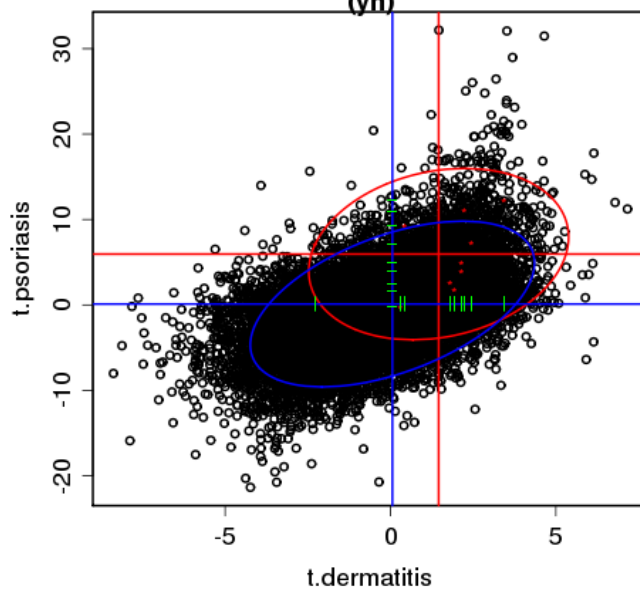
GO:0046034
ATP metabolic process
(yh)



GO:0044265
cellular macromolecule catabolic process
(yh)



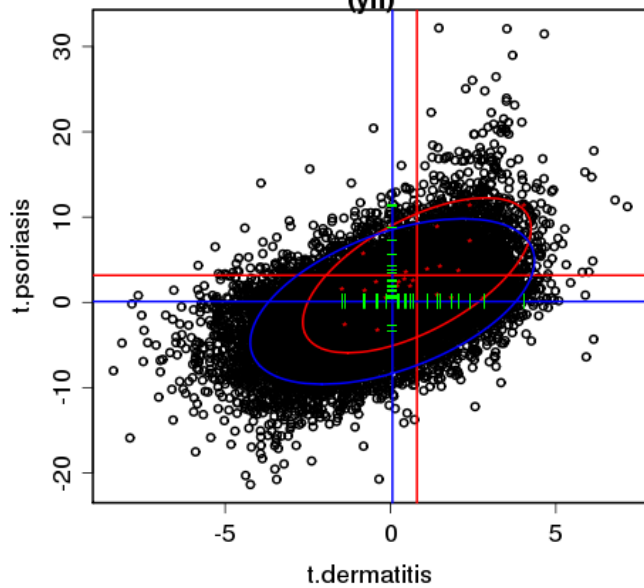
GO:0045840
positive regulation of mitosis
(yh)



GO:0001906

cell killing

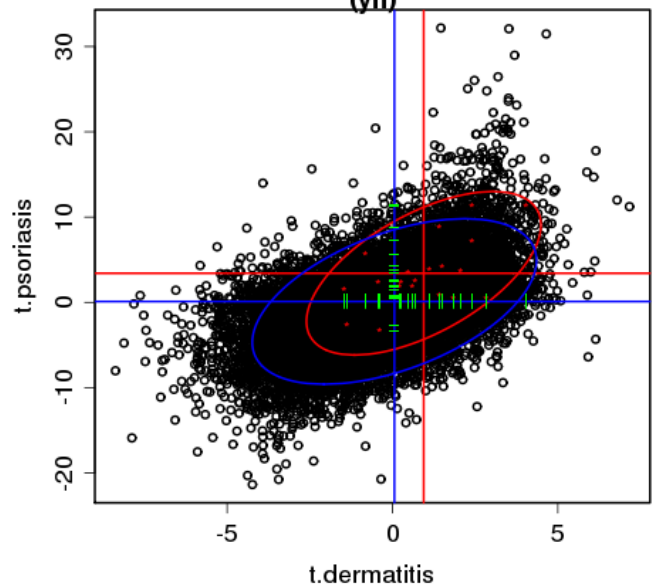
(yh)



GO:0001909

leukocyte mediated cytotoxicity

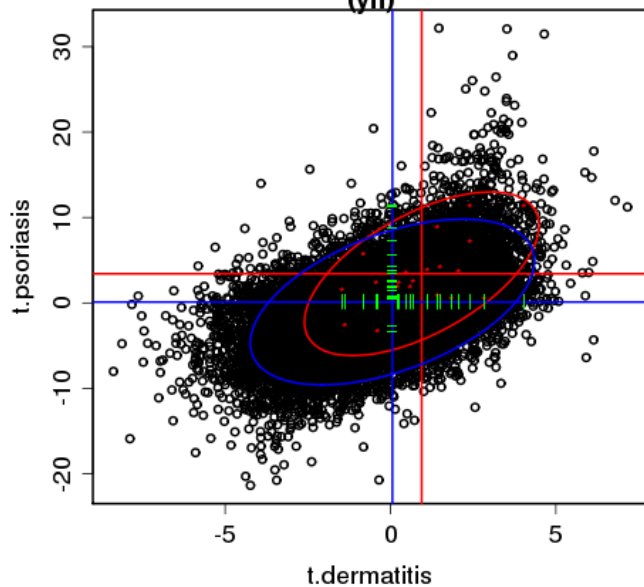
(yh)



GO:0002228

natural killer cell mediated immunity

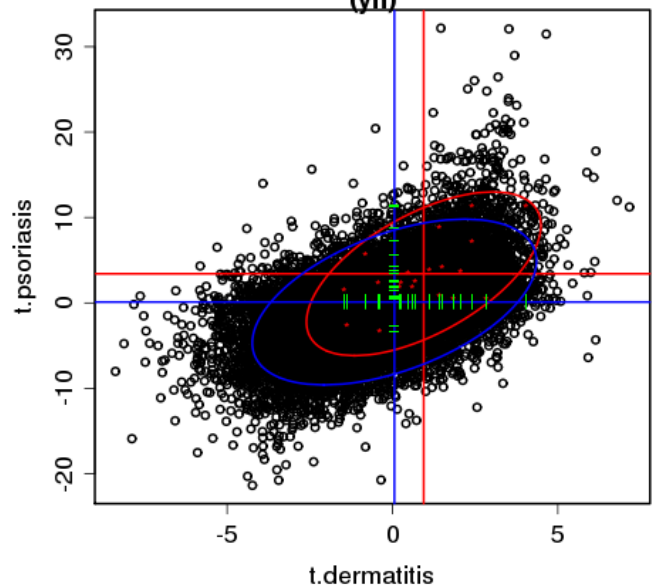
(yh)



GO:0042267

natural killer cell mediated cytotoxicity

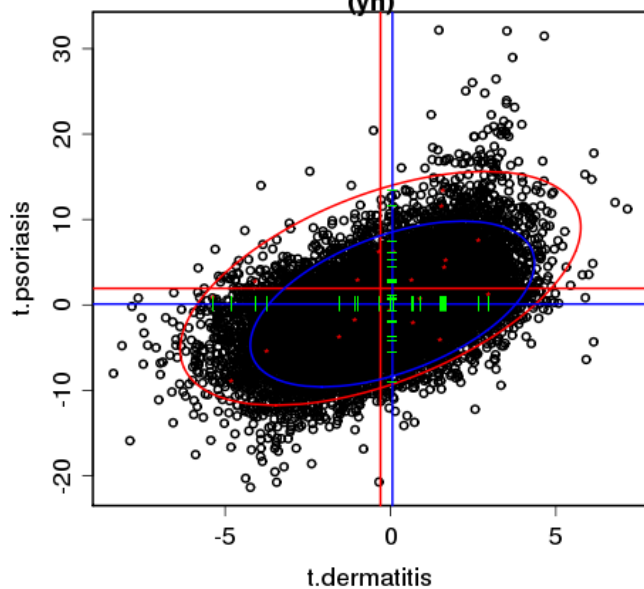
(yh)



GO:0006984

ER-nuclear signaling pathway

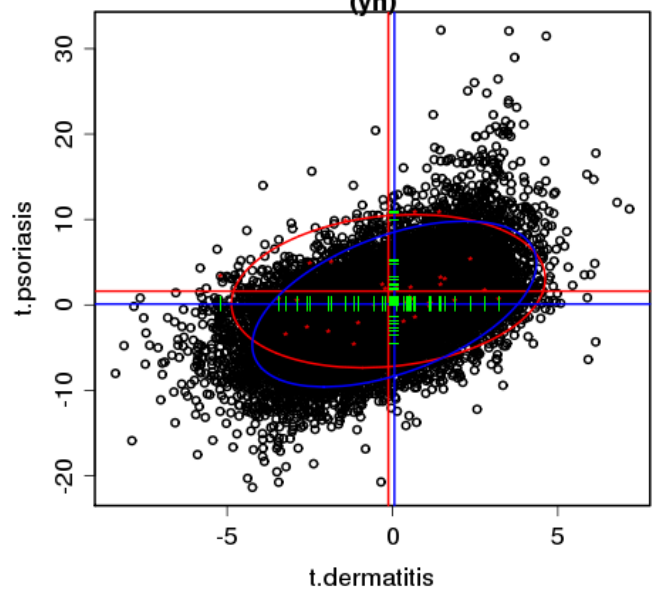
(yh)

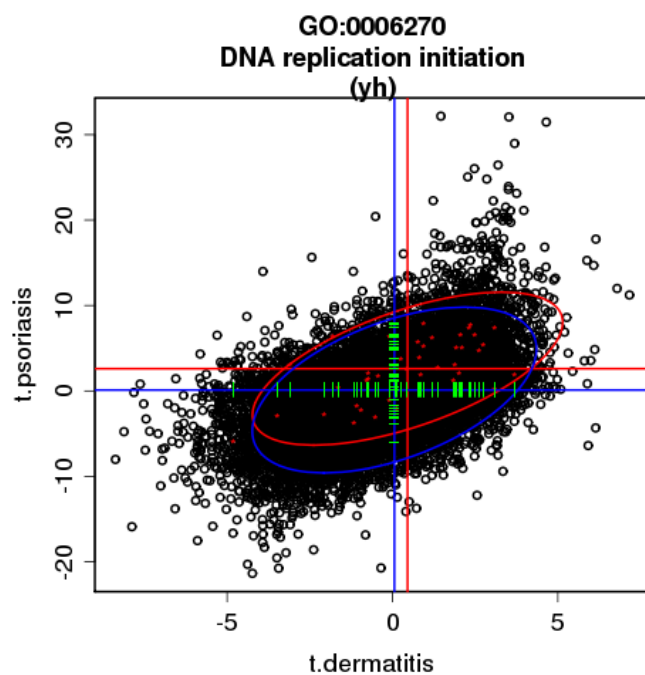
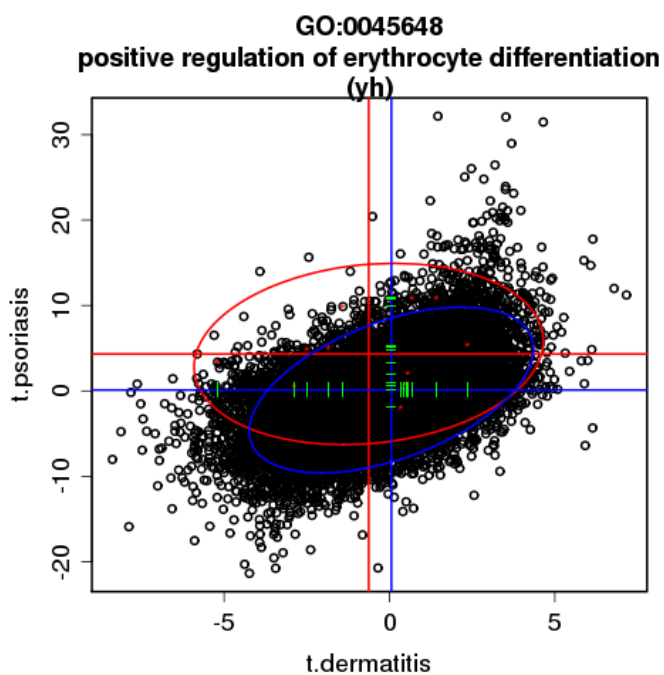
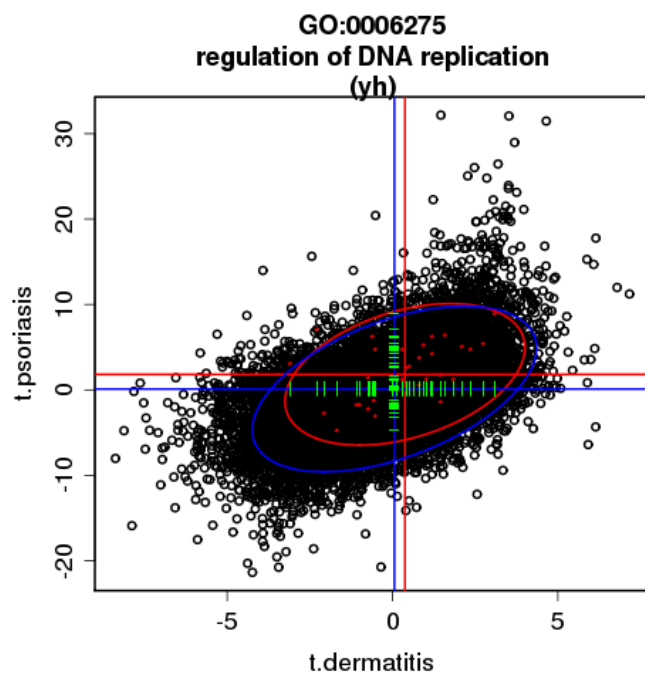
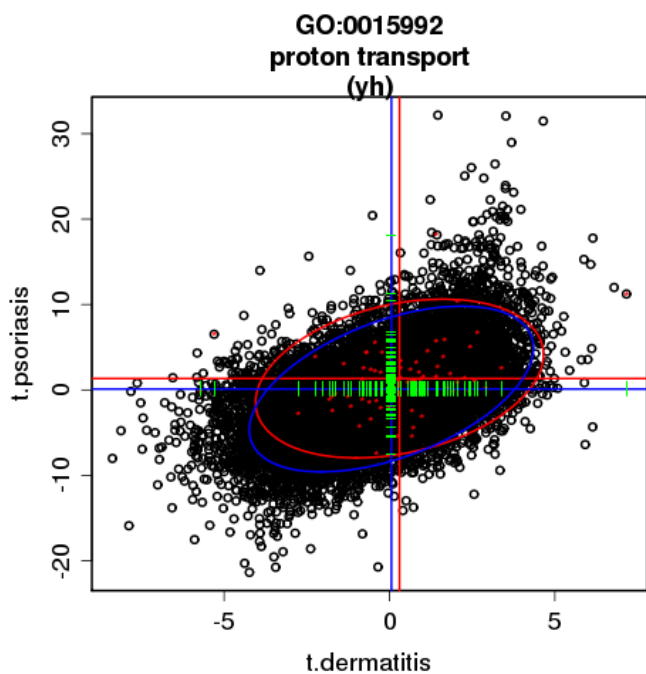
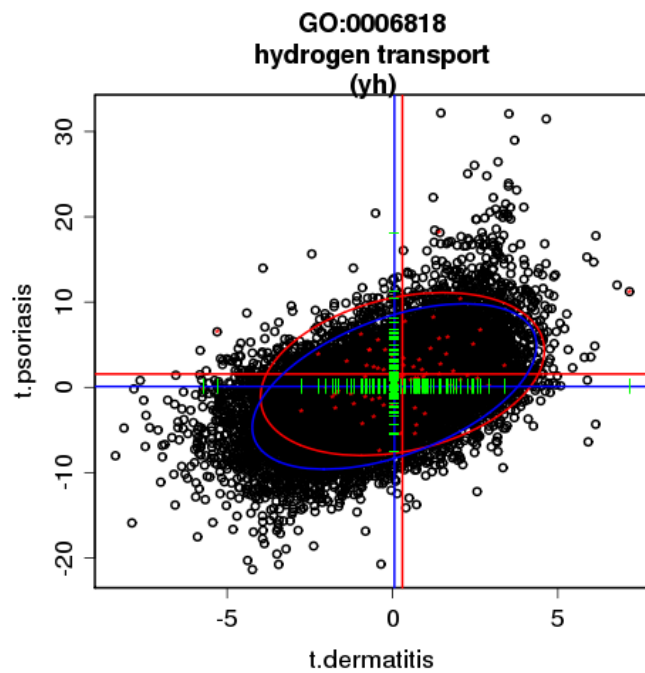
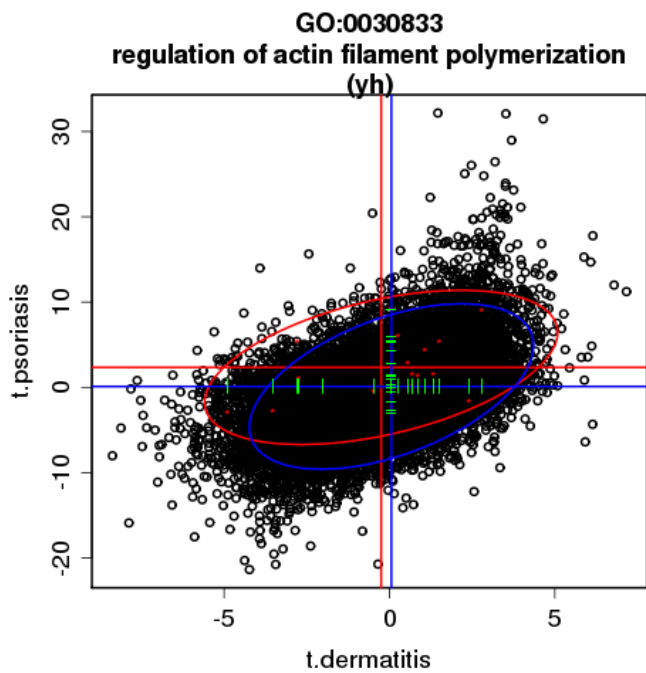


GO:0045639

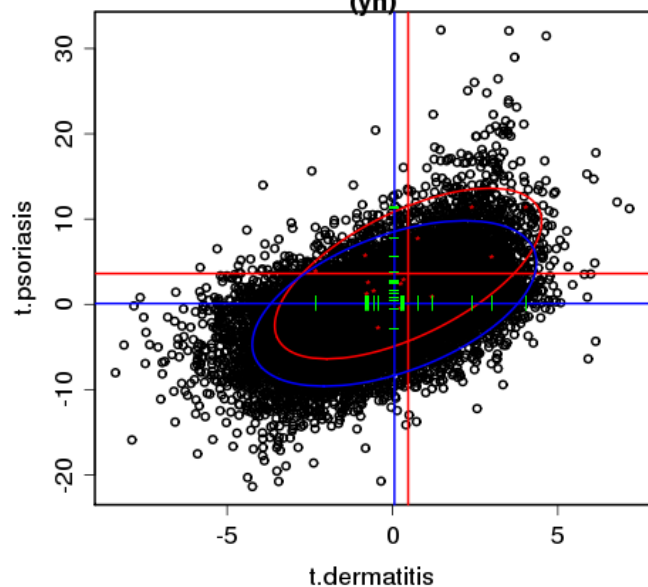
positive regulation of myeloid cell differentiation

(yh)

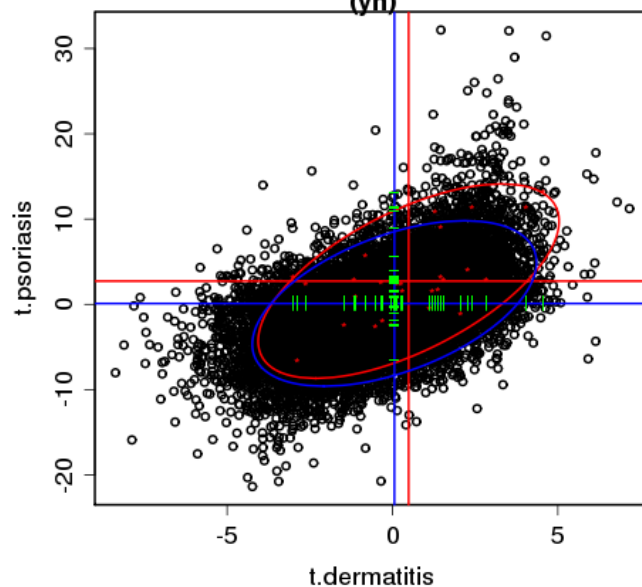




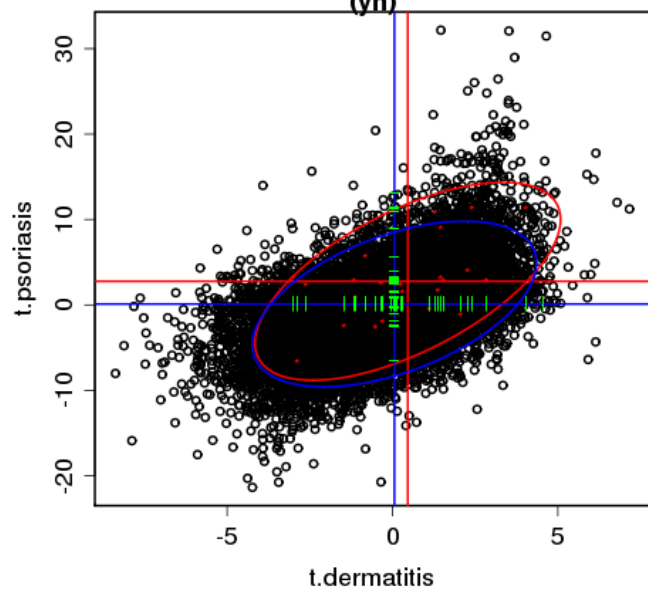
GO:0002456
T cell mediated immunity
(yh)



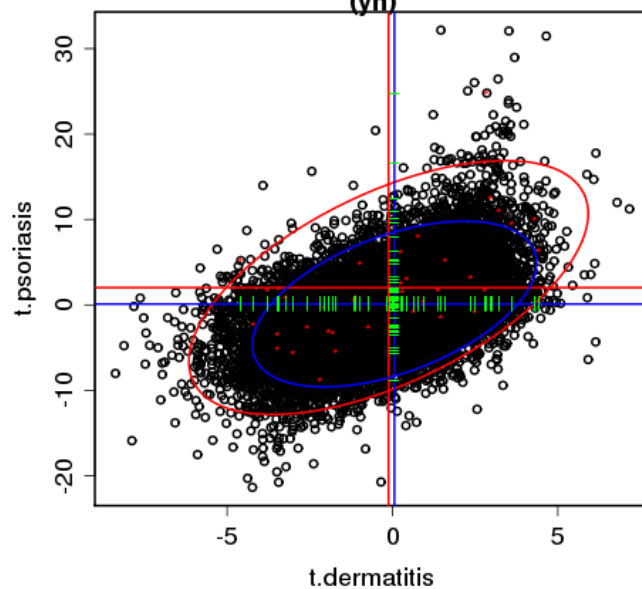
GO:0051648
vesicle localization
(yh)



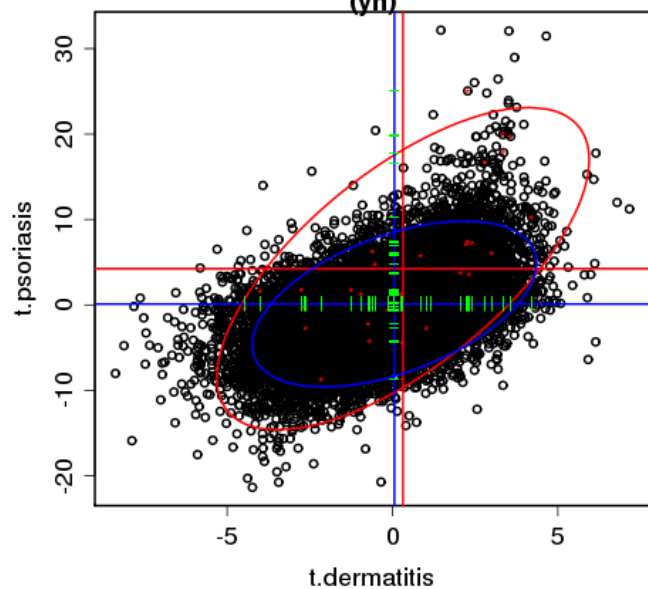
GO:0051650
establishment of vesicle localization
(yh)



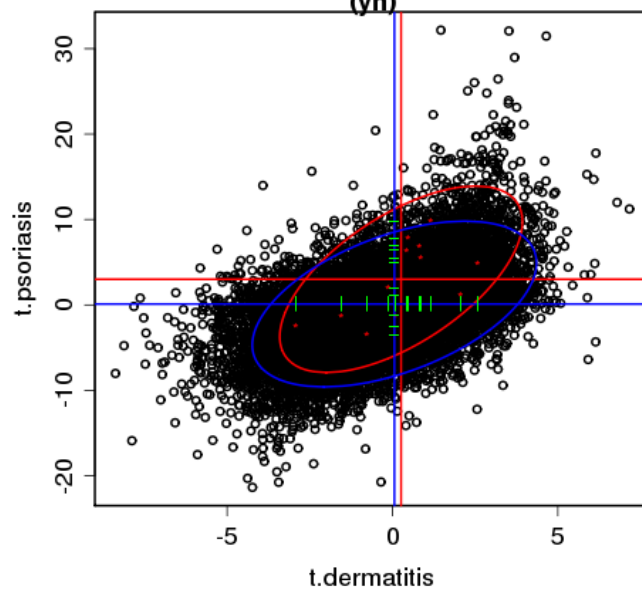
GO:0048730
epidermis morphogenesis
(yh)

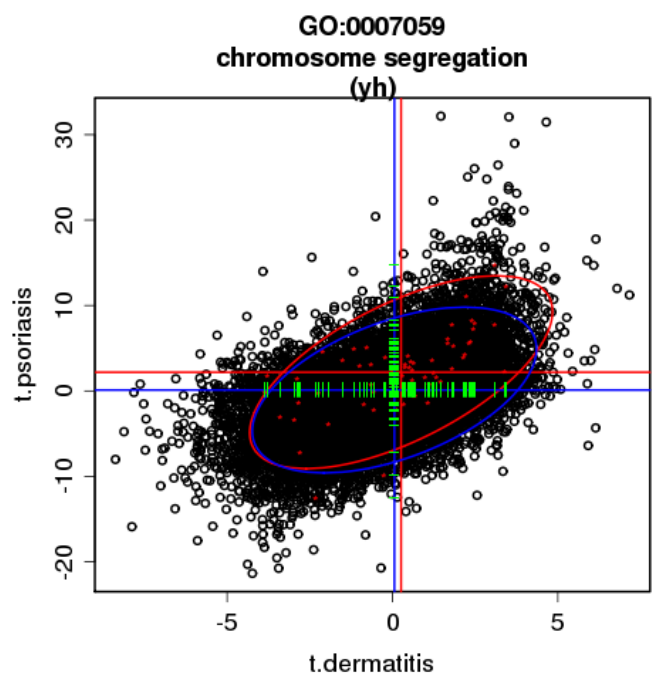
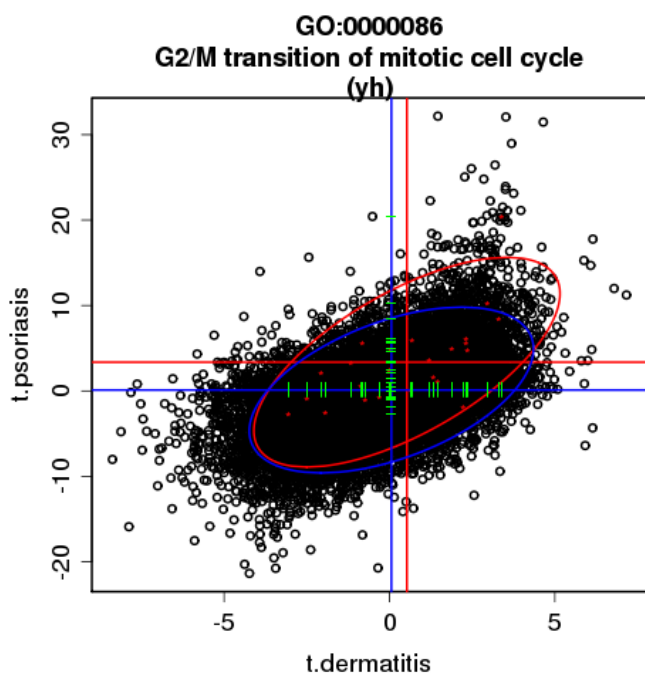
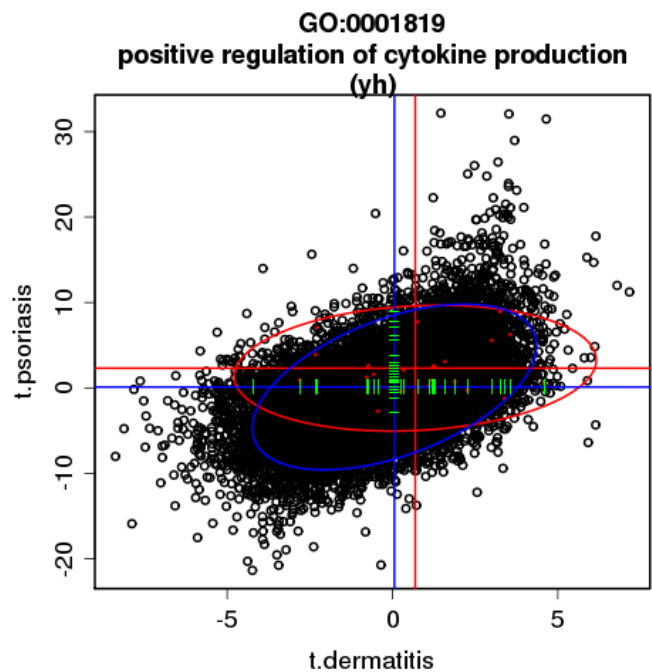
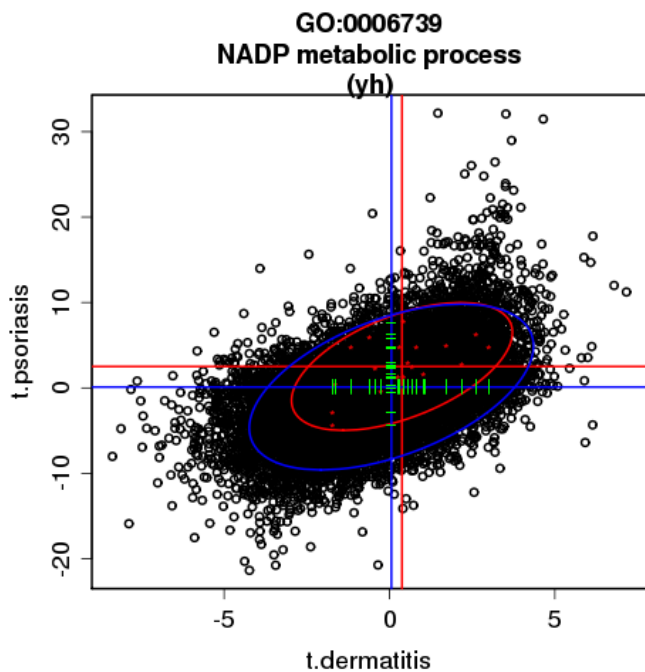
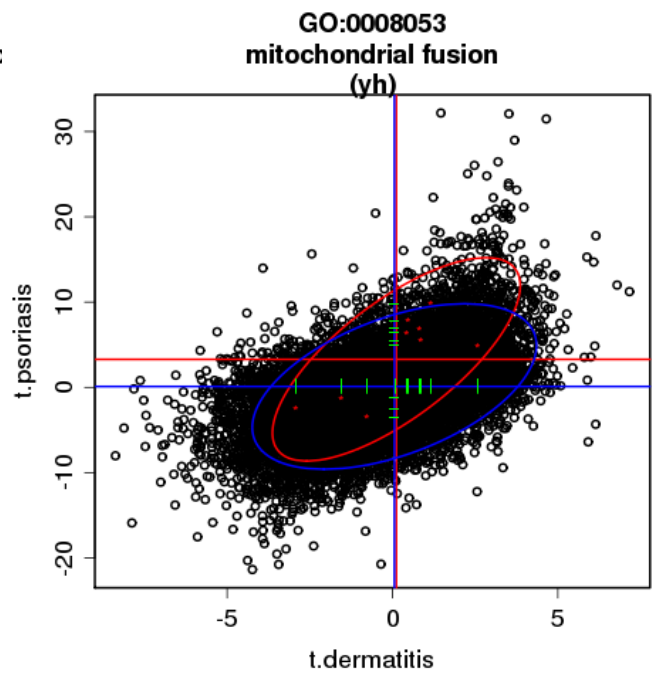
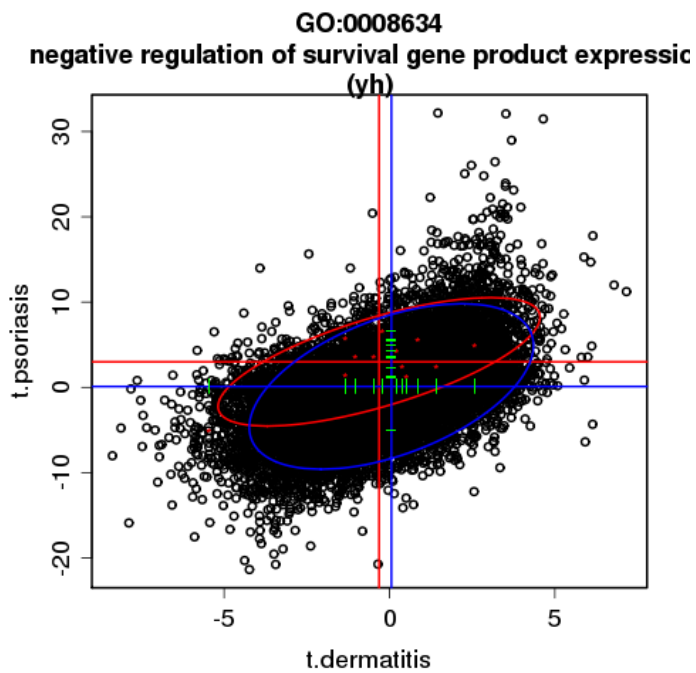


GO:0009411
response to UV
(yh)

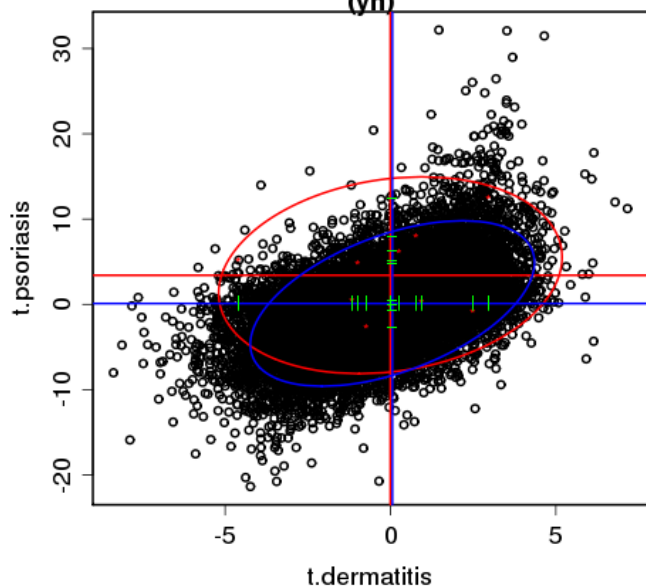


GO:0048284
organelle fusion
(yh)

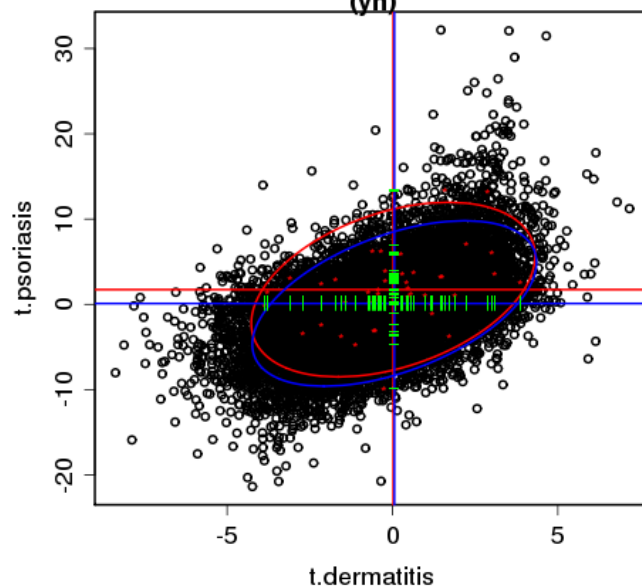




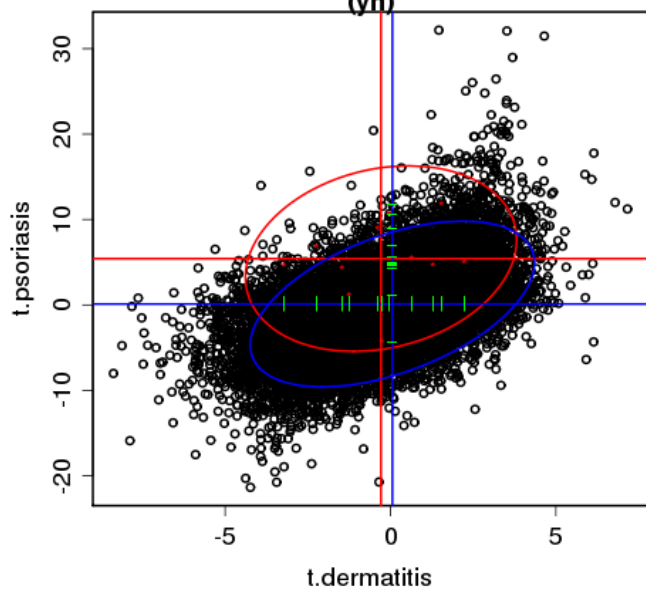
GO:0031069
hair follicle morphogenesis
(yh)



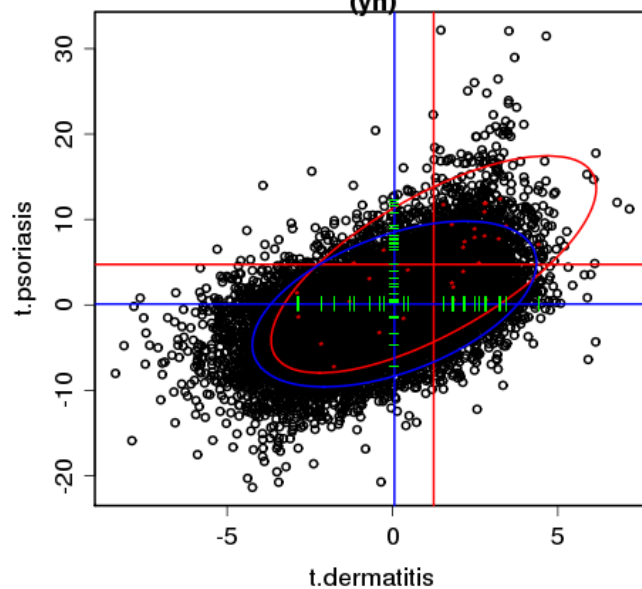
GO:0006302
double-strand break repair
(yh)



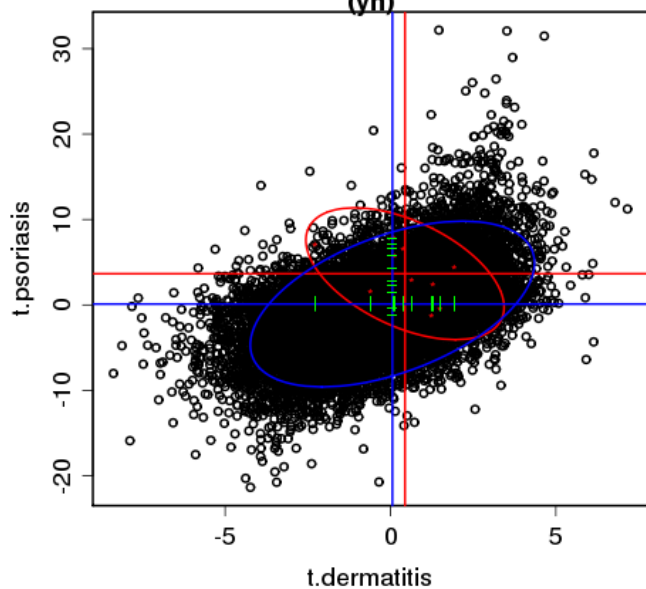
GO:0007032
endosome organization and biogenesis
(yh)



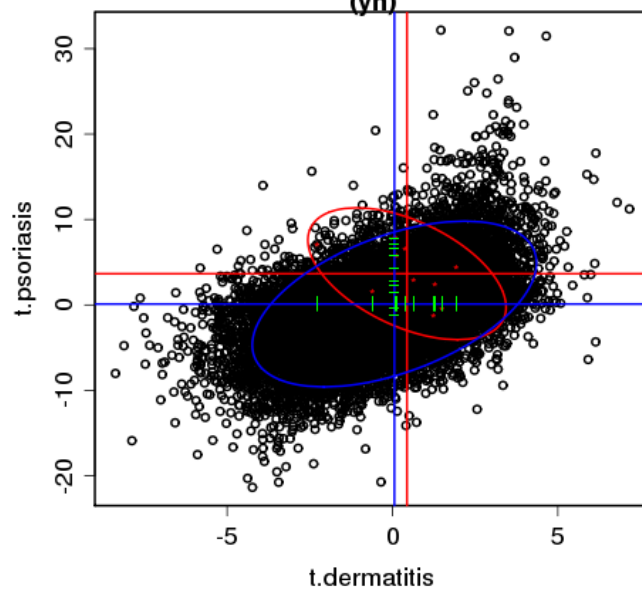
GO:0007051
spindle organization and biogenesis
(yh)



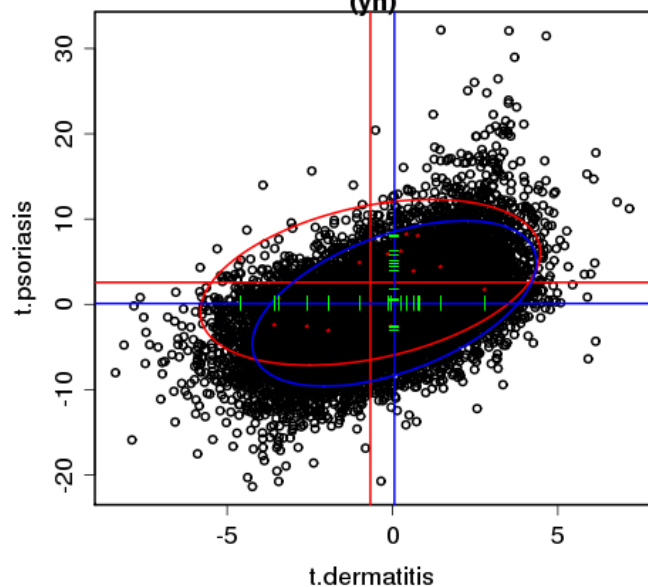
GO:0032635
interleukin-6 production
(yh)



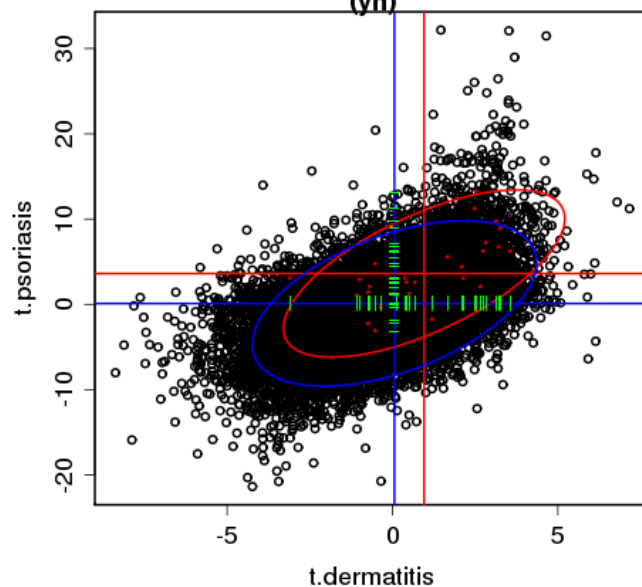
GO:0042226
interleukin-6 biosynthetic process
(yh)



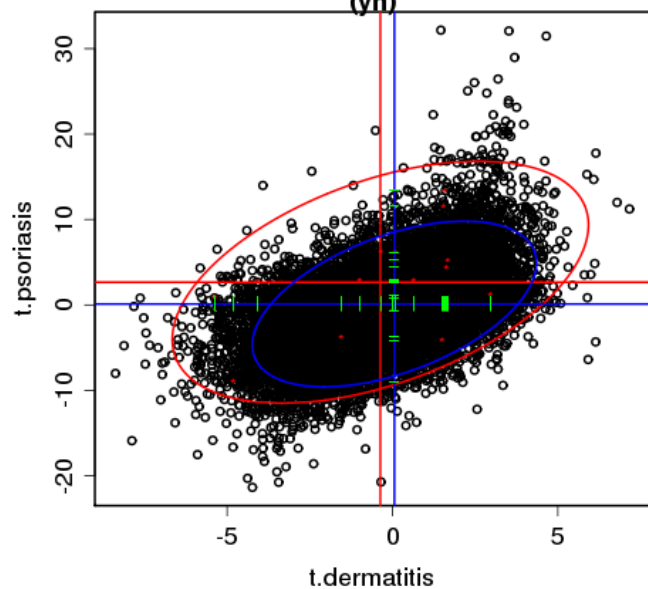
GO:0008593
regulation of Notch signaling pathway
(yh)



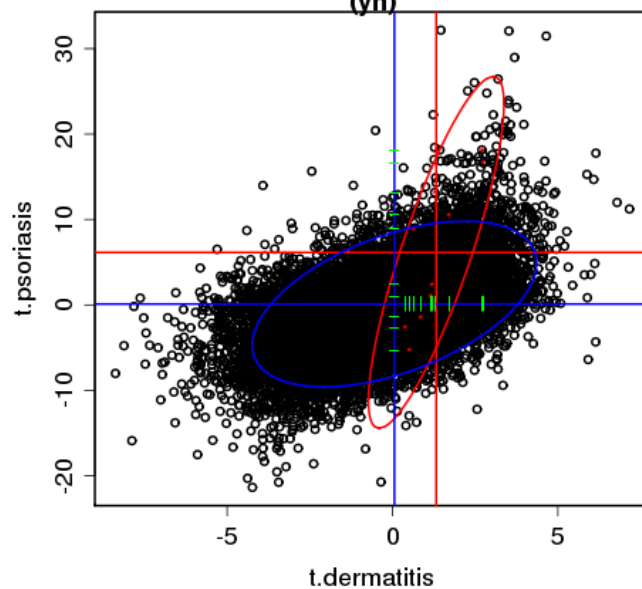
GO:0030330
A damage response, signal transduction by p53 class m
(yh)



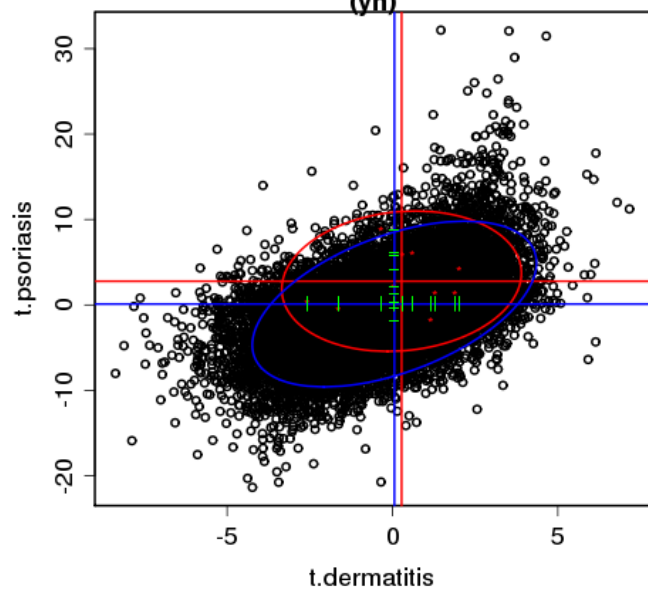
GO:0030968
endoplasmic reticulum unfolded protein response
(yh)



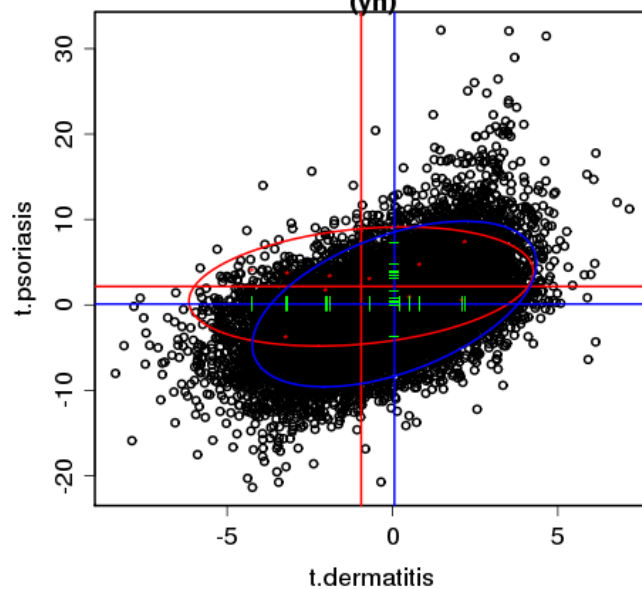
GO:0046479
glycosphingolipid catabolic process
(yh)



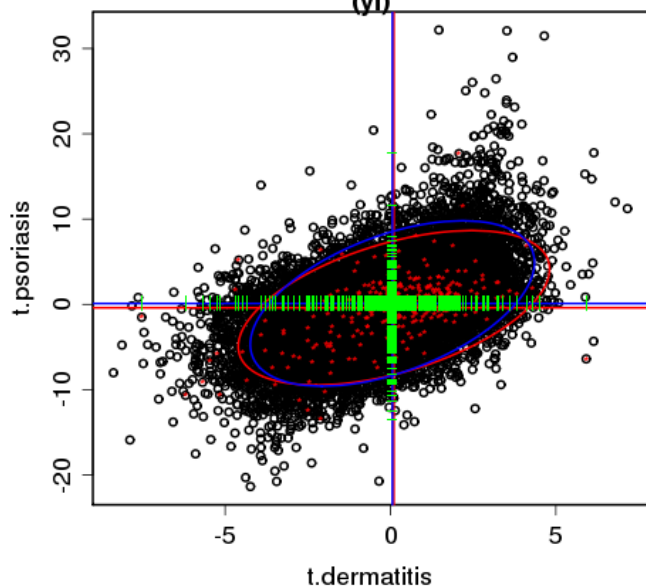
GO:0006829
zinc ion transport
(yh)



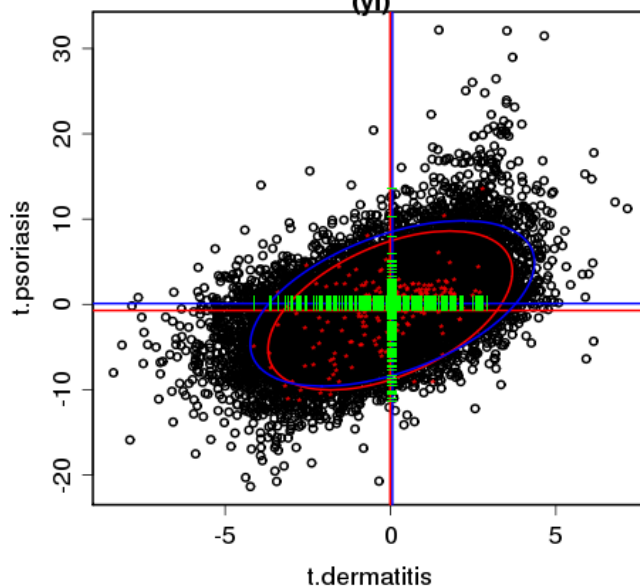
GO:0007020
microtubule nucleation
(yh)



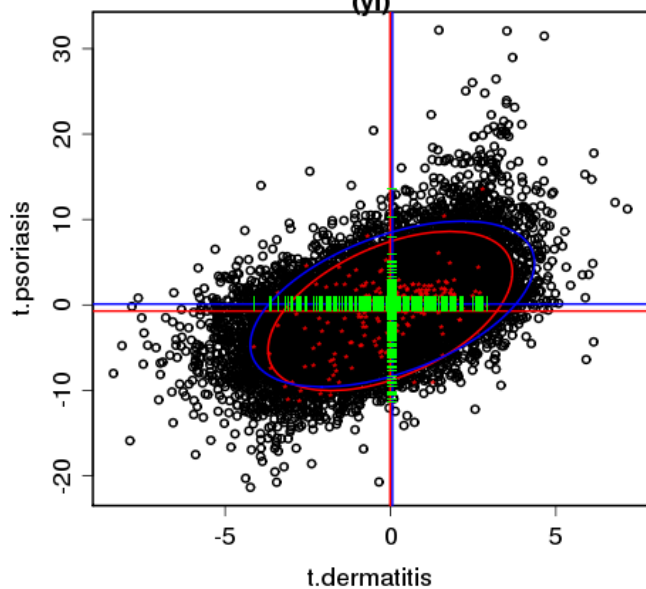
GO:0001501
skeletal development
(yl)



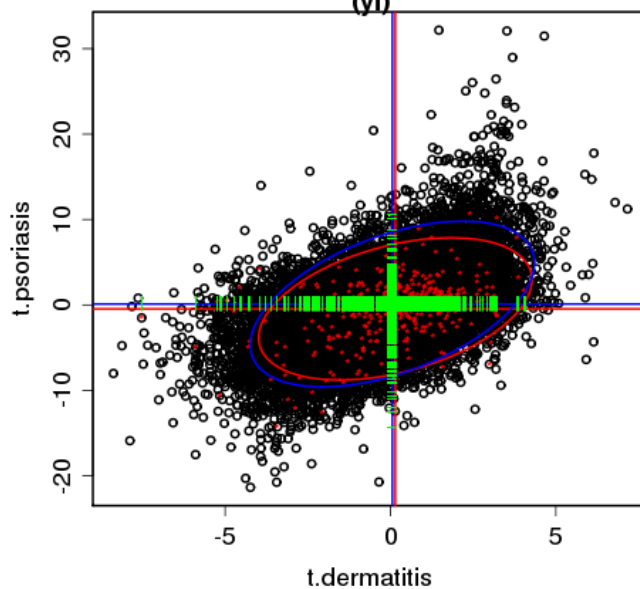
GO:0003012
muscle system process
(yl)



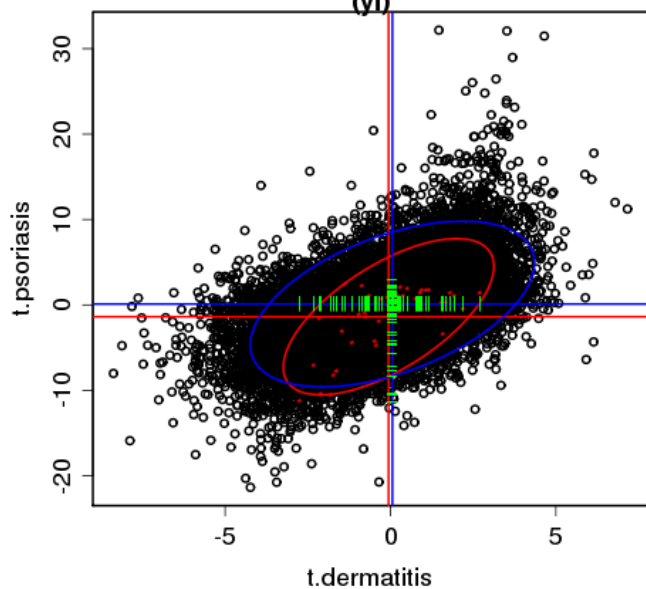
GO:0006936
muscle contraction
(yl)



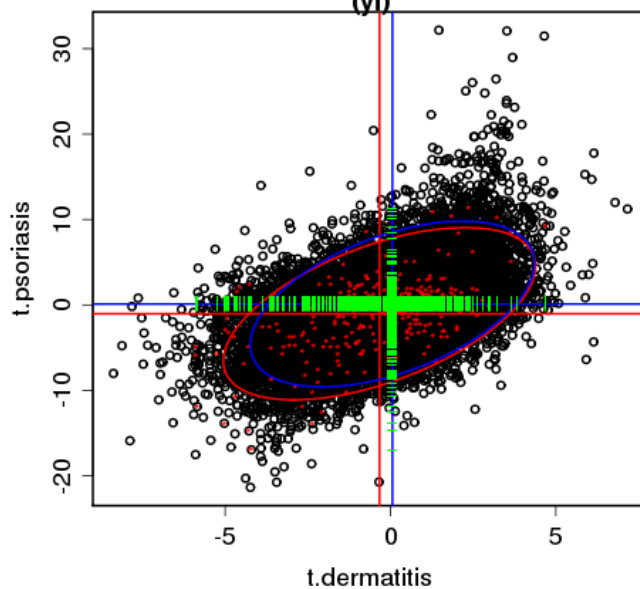
GO:0019226
transmission of nerve impulse
(yl)



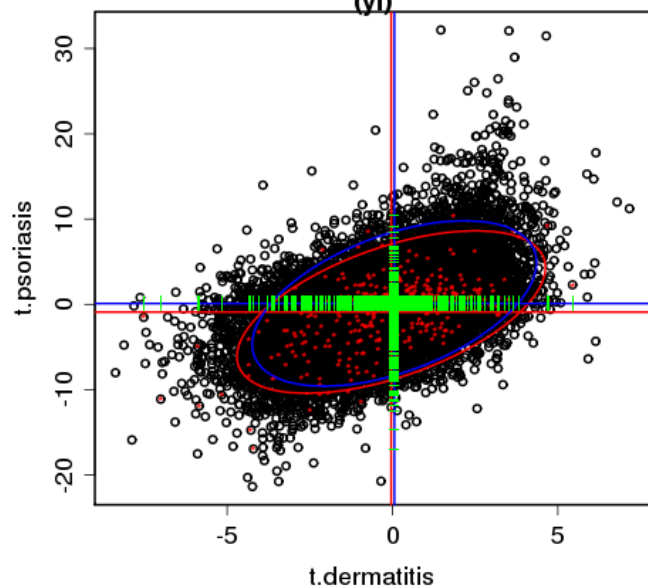
GO:0006939
smooth muscle contraction
(yl)



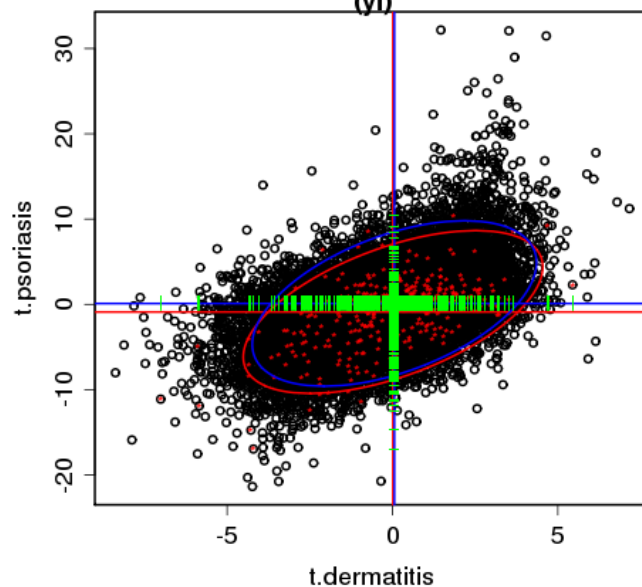
GO:0007417
central nervous system development
(yl)



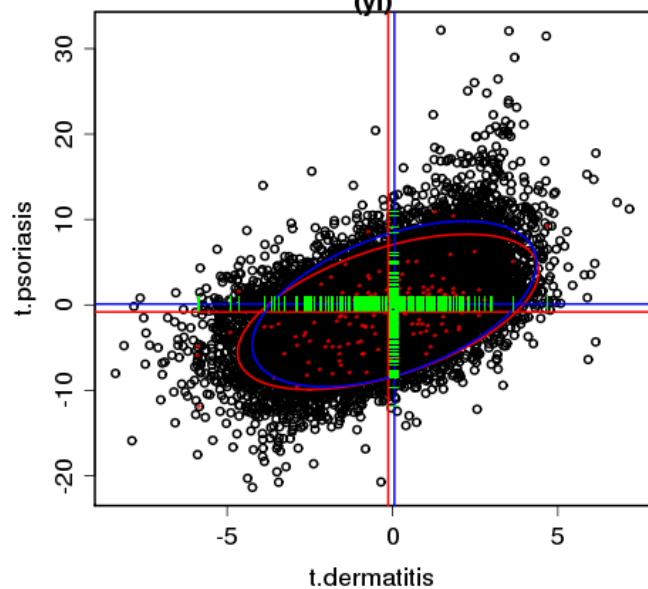
GO:0022008
neurogenesis
(yl)



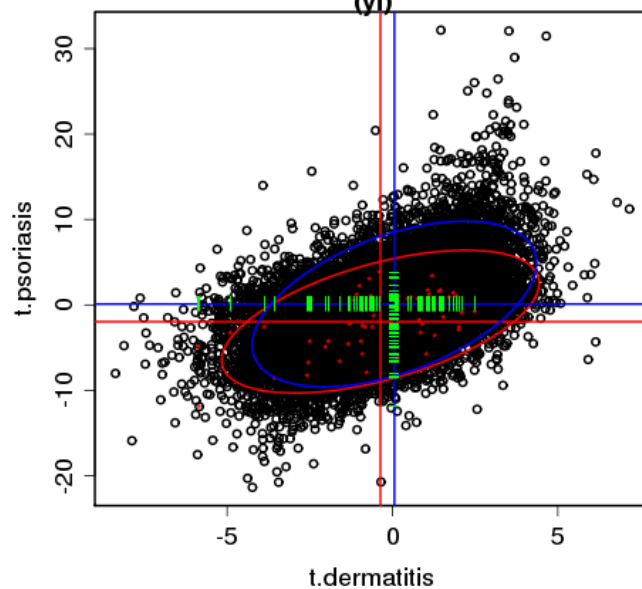
GO:0048699
generation of neurons
(yl)



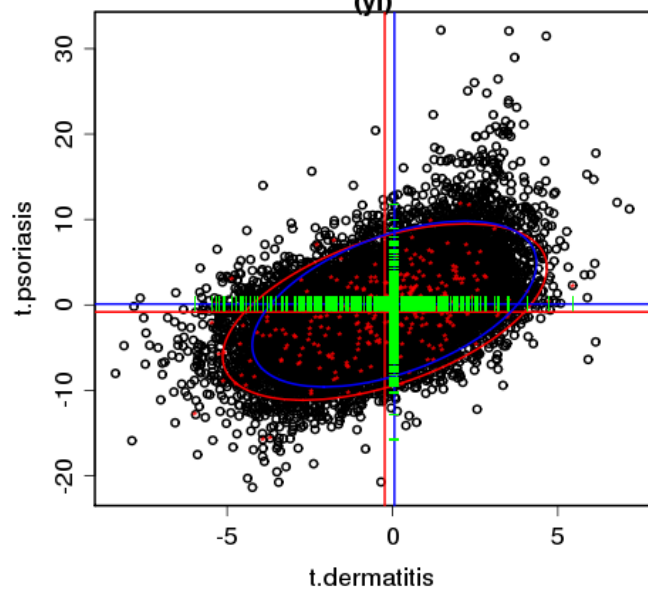
GO:0007420
brain development
(yl)



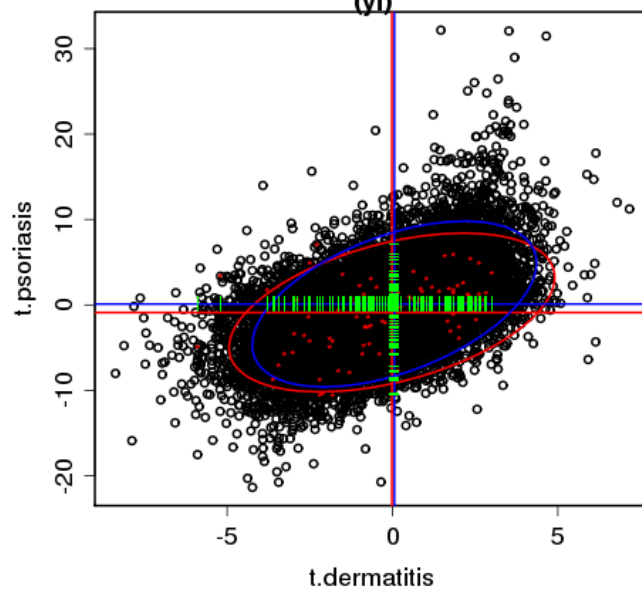
GO:0030900
forebrain development
(yl)



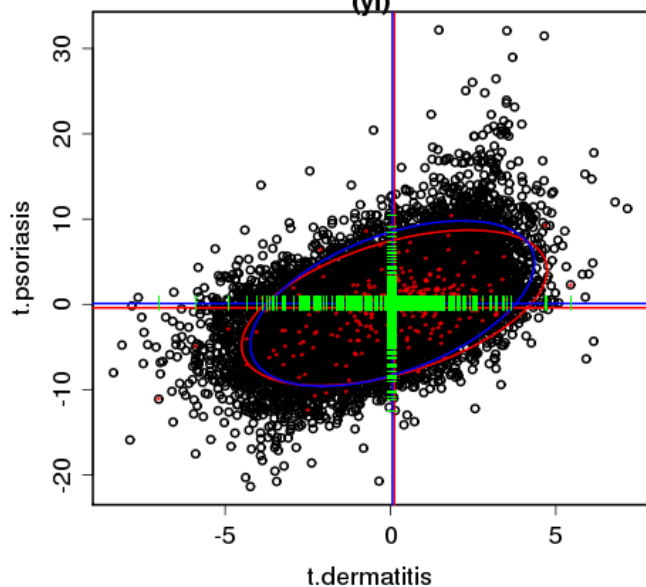
GO:0008285
negative regulation of cell proliferation
(yl)



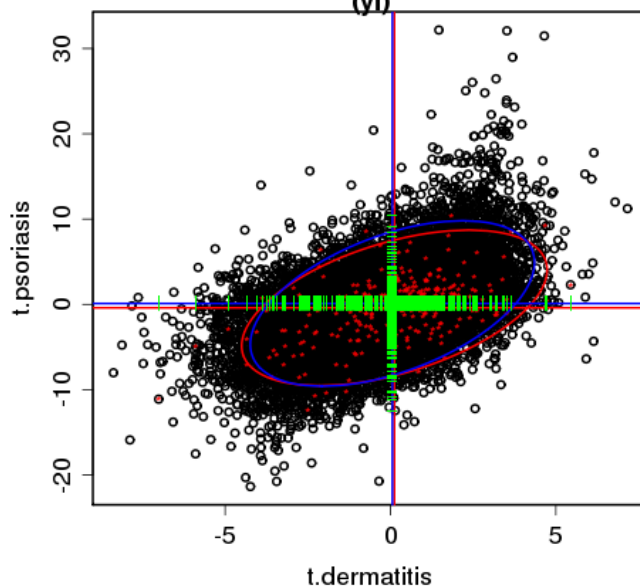
GO:0021700
developmental maturation
(yl)



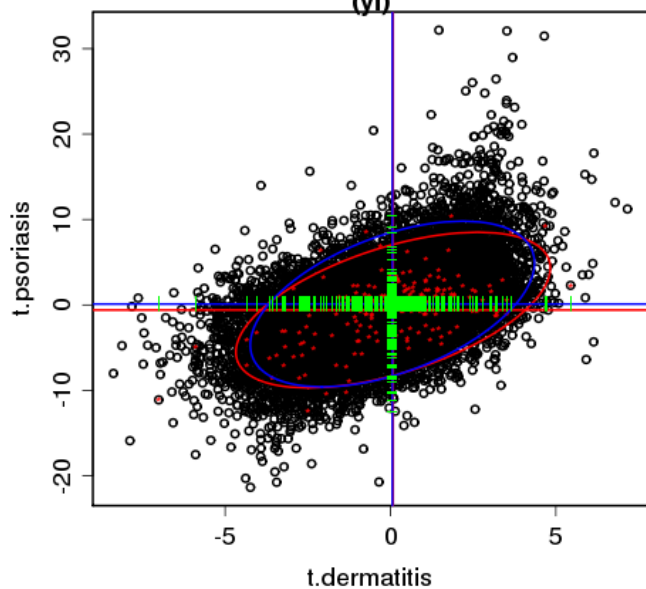
GO:0032990
cell part morphogenesis
(yl)



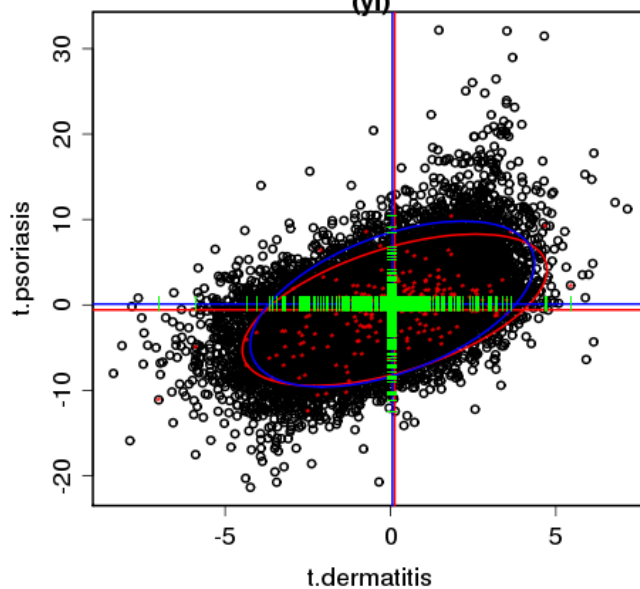
GO:0030030
cell projection organization and biogenesis
(yl)



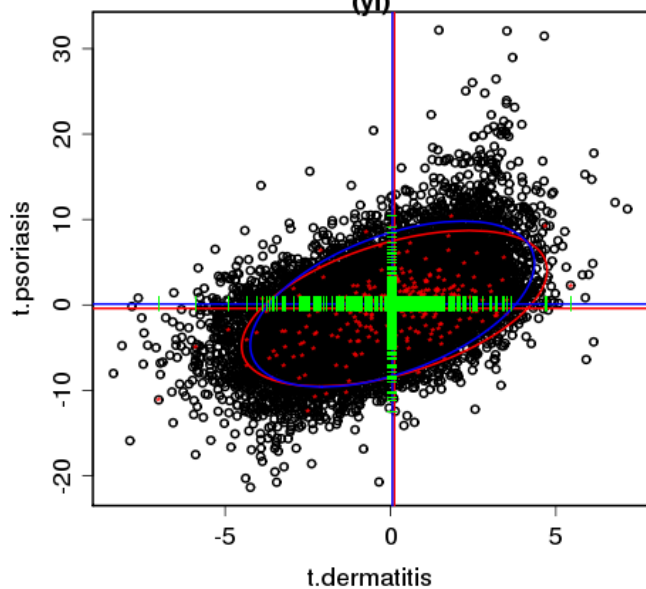
GO:0031175
neurite development
(yl)



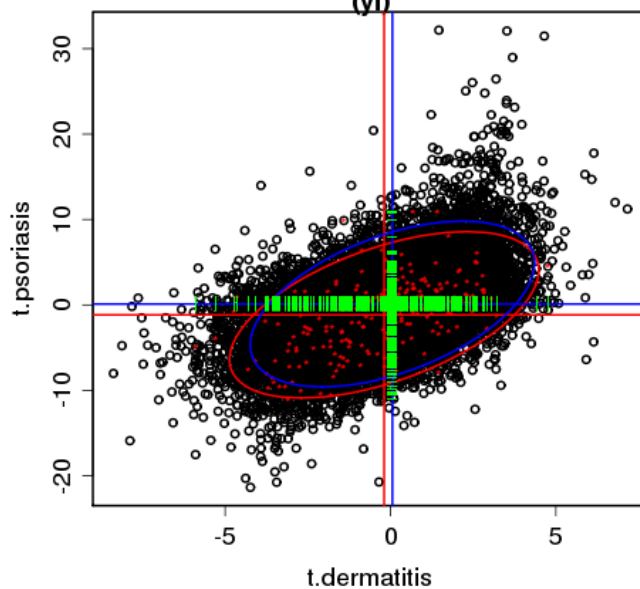
GO:0048666
neuron development
(yl)



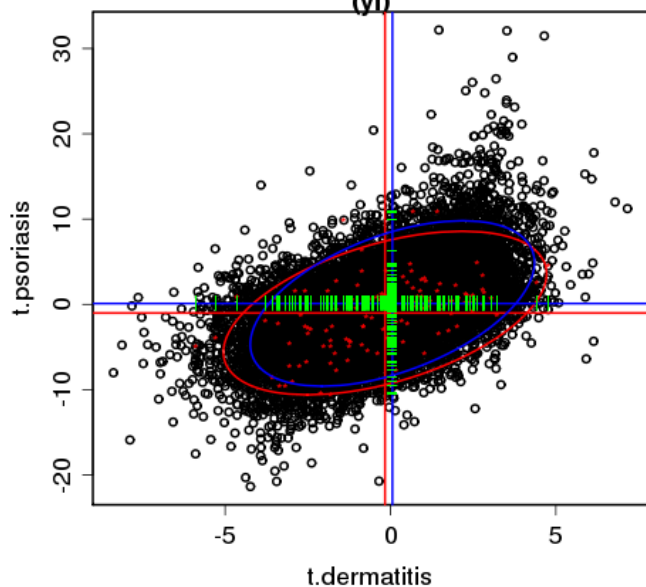
GO:0048858
cell projection morphogenesis
(yl)



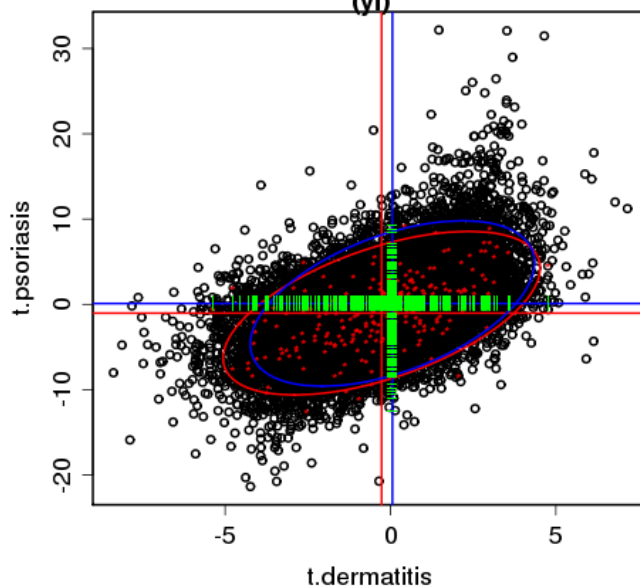
GO:0007517
muscle development
(yl)



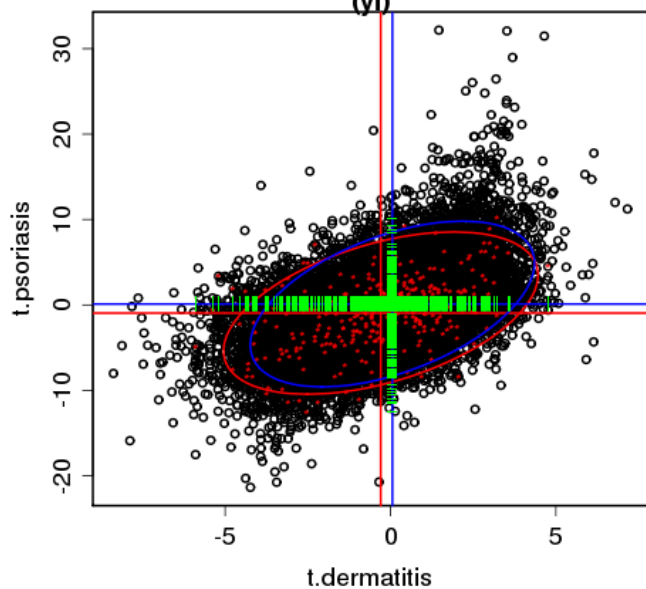
GO:0014706
striated muscle development
(yl)



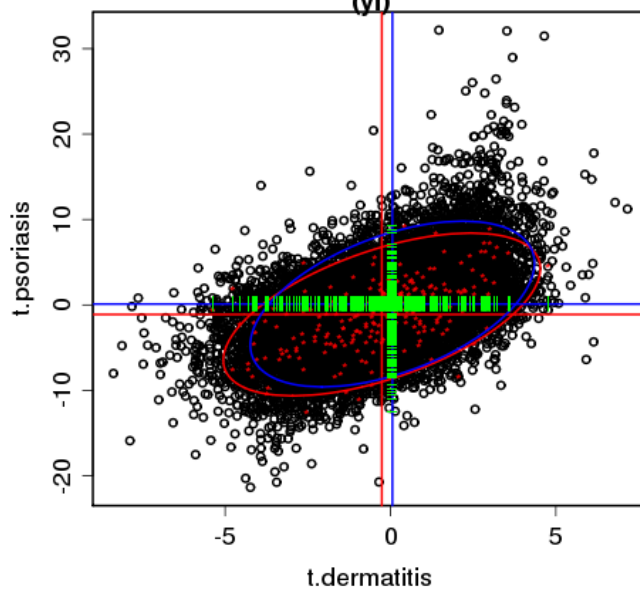
GO:0008361
regulation of cell size
(yl)



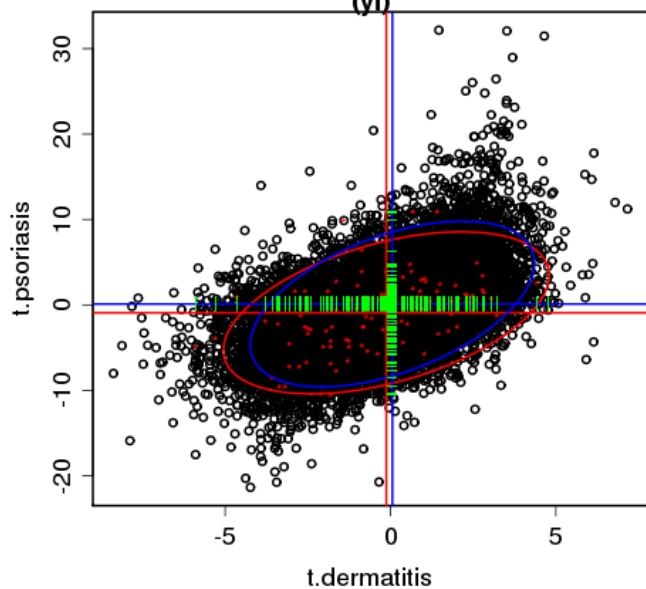
GO:0040007
growth
(yl)



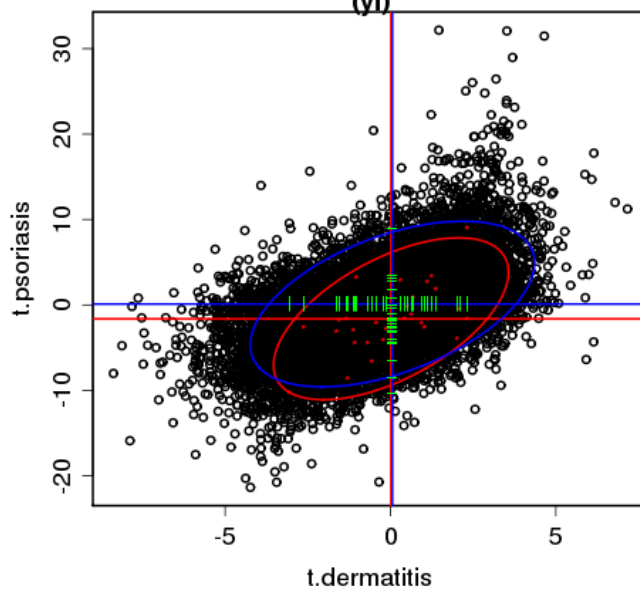
GO:0016049
cell growth
(yl)

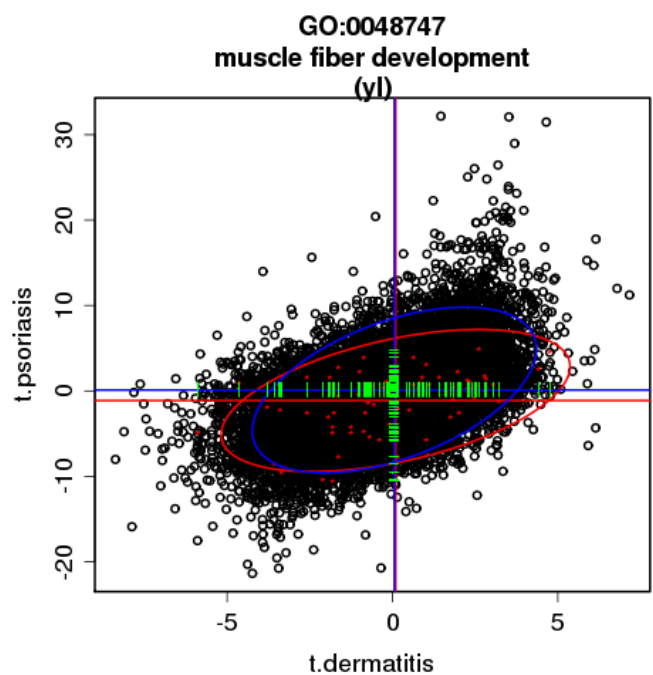
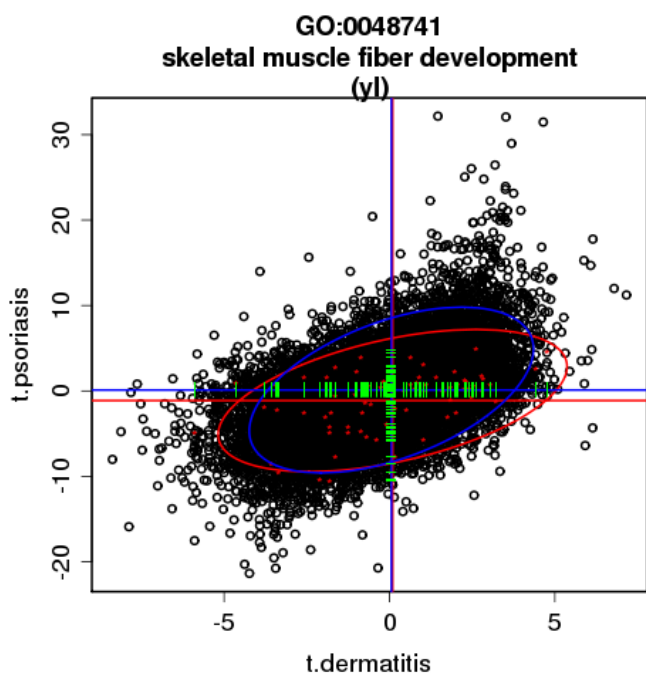
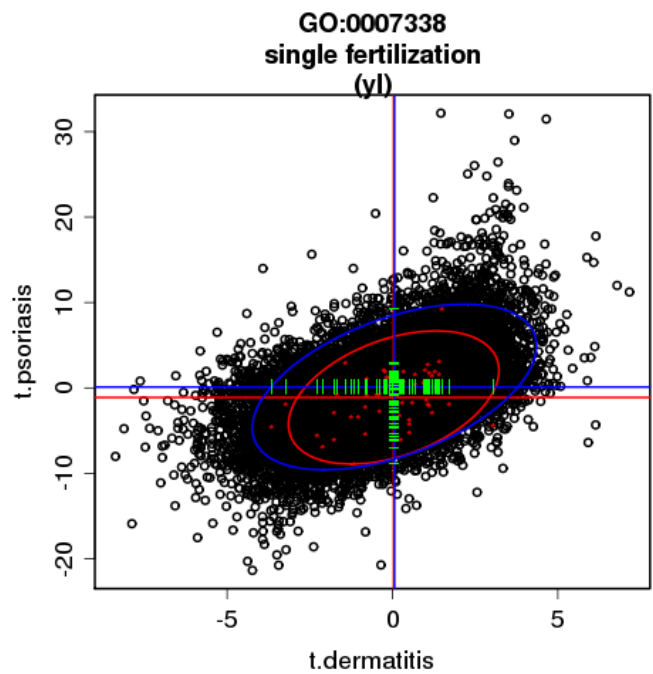
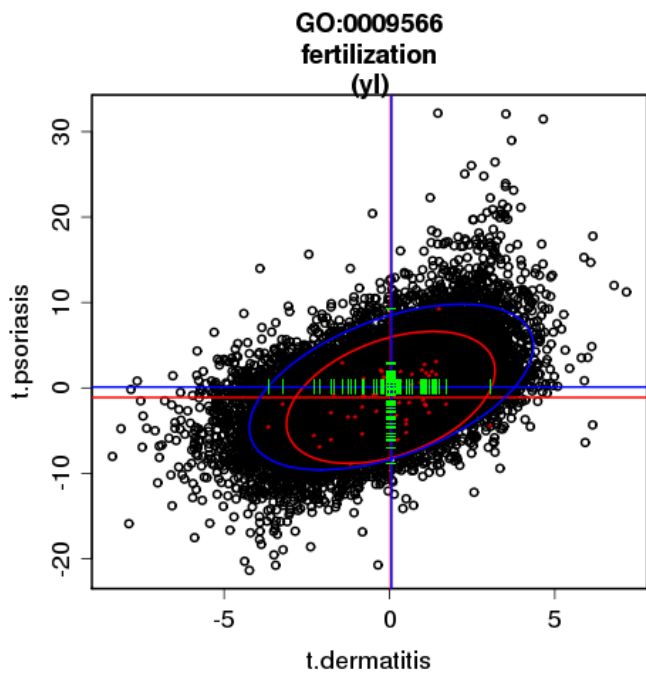
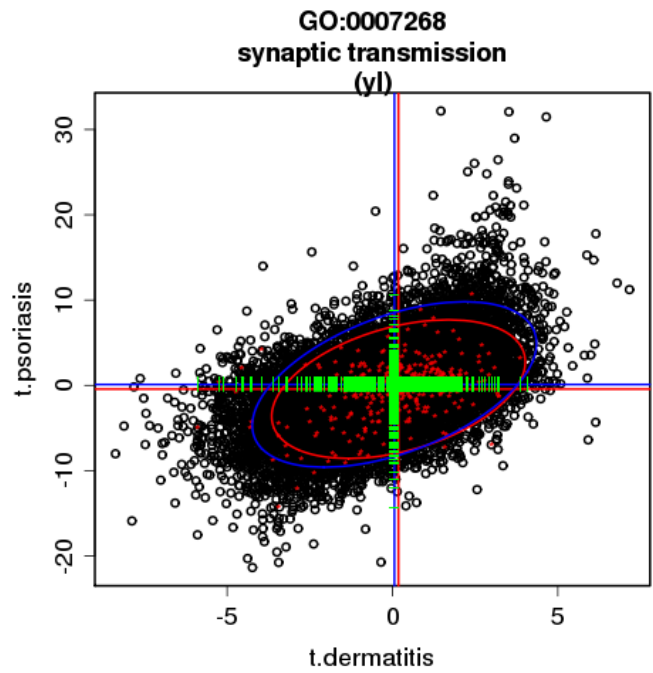
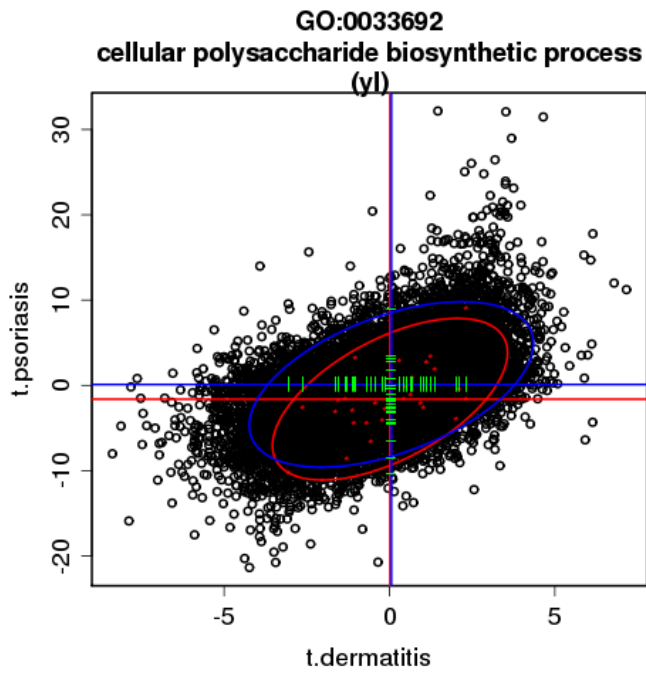


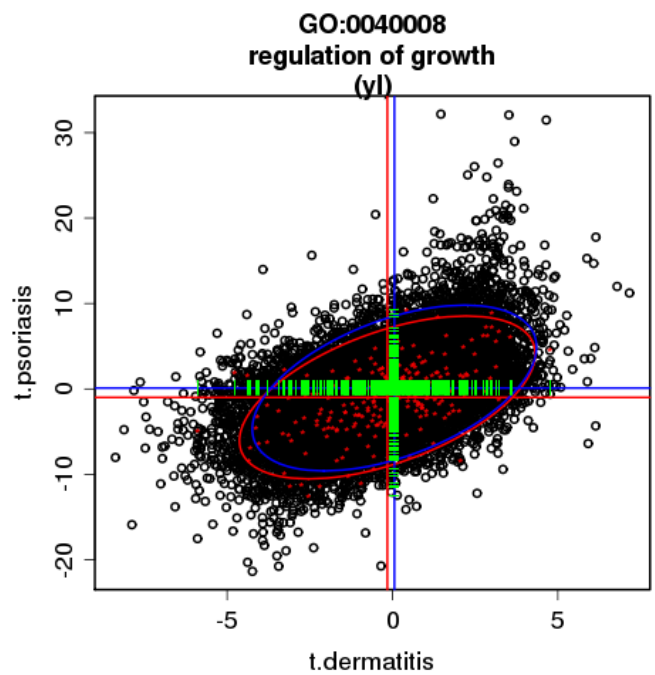
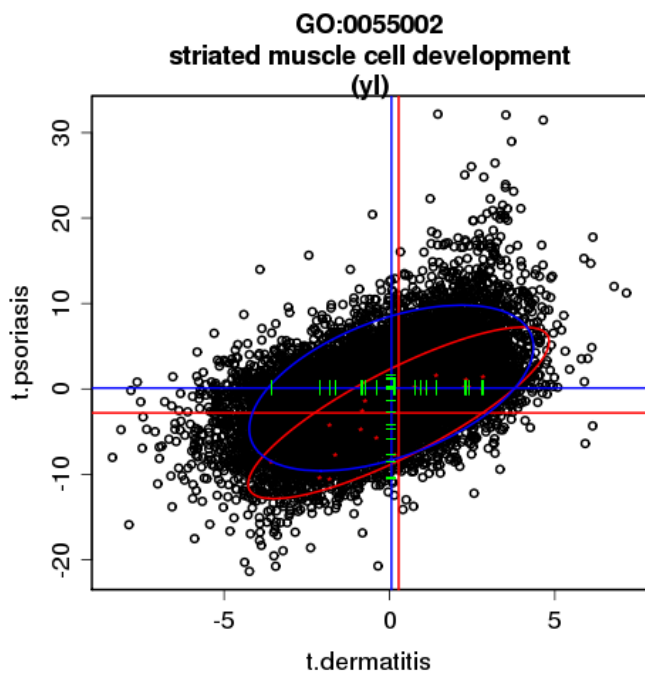
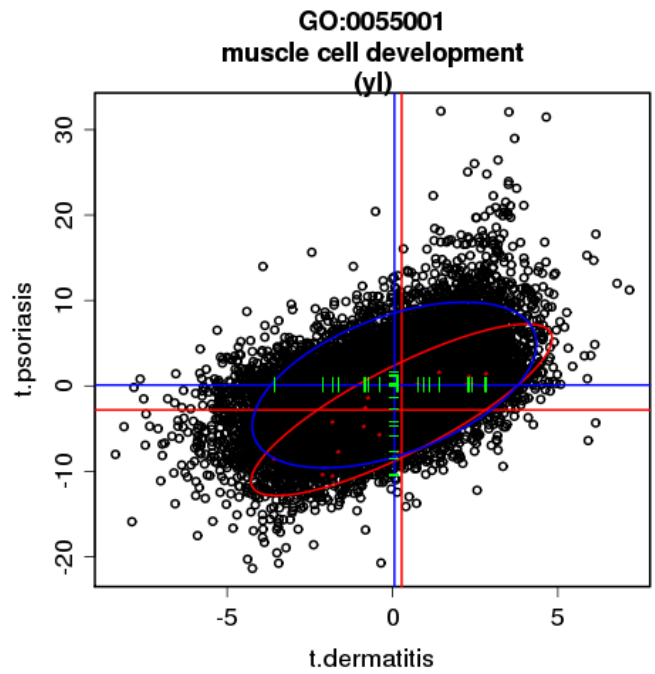
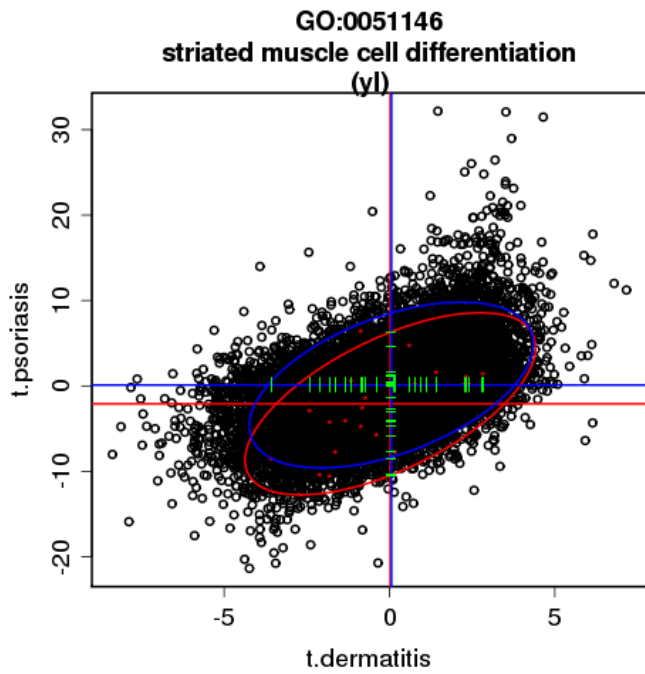
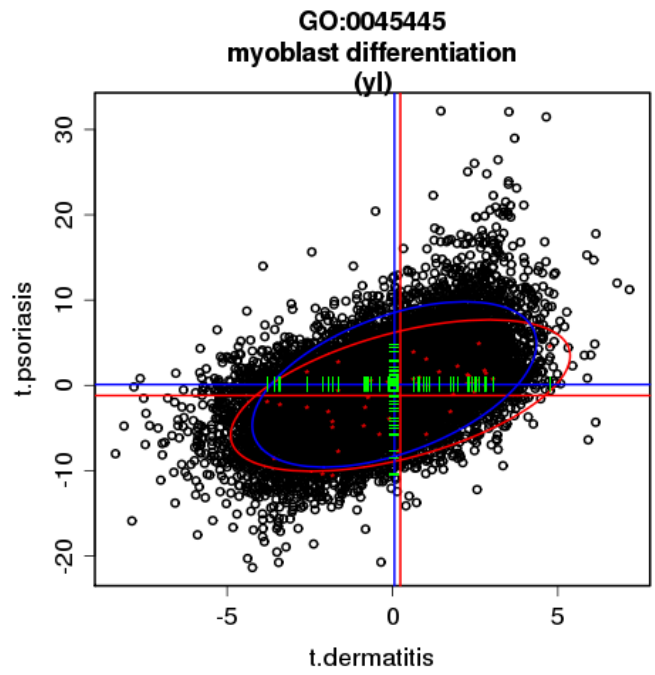
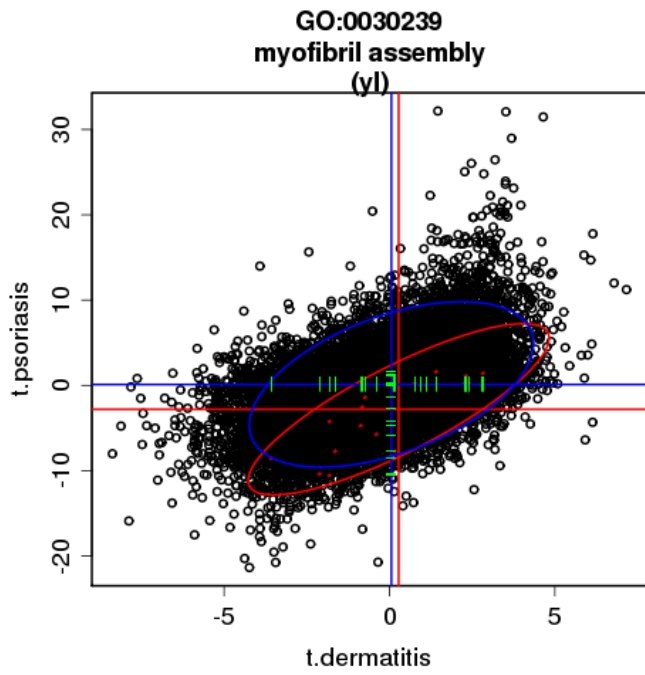
GO:0007519
skeletal muscle development
(yl)

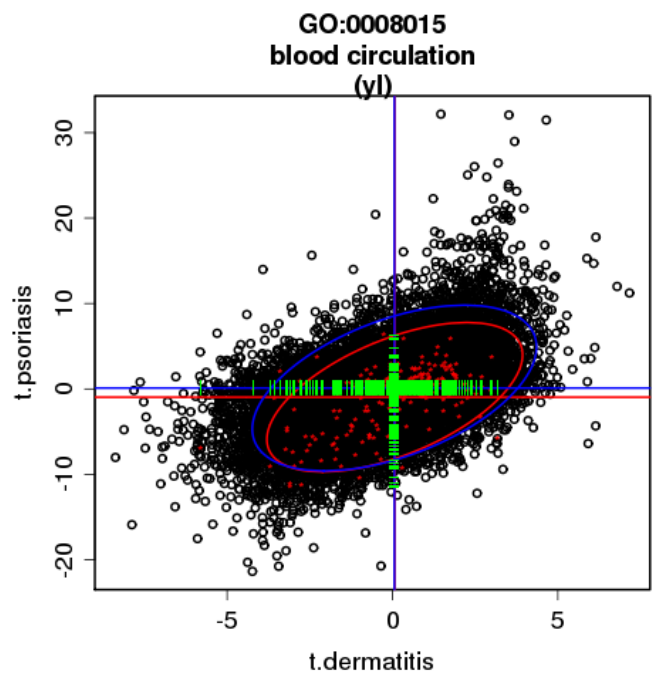
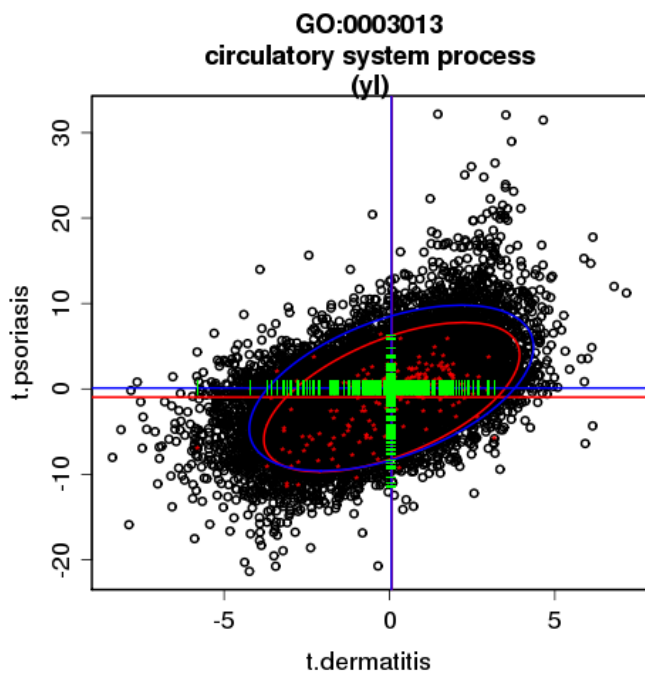
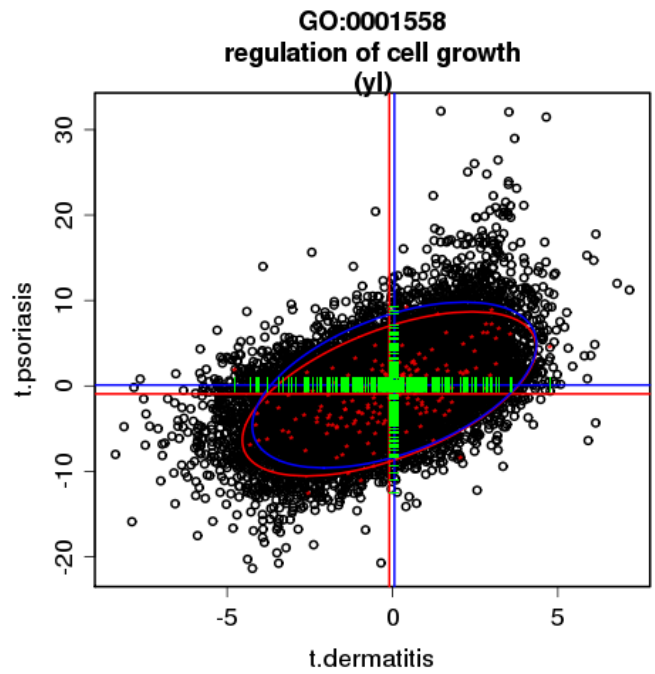
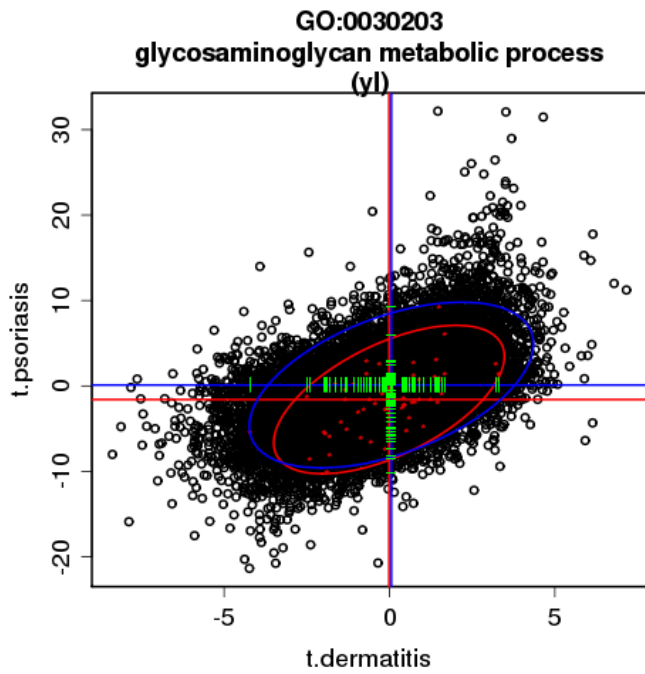
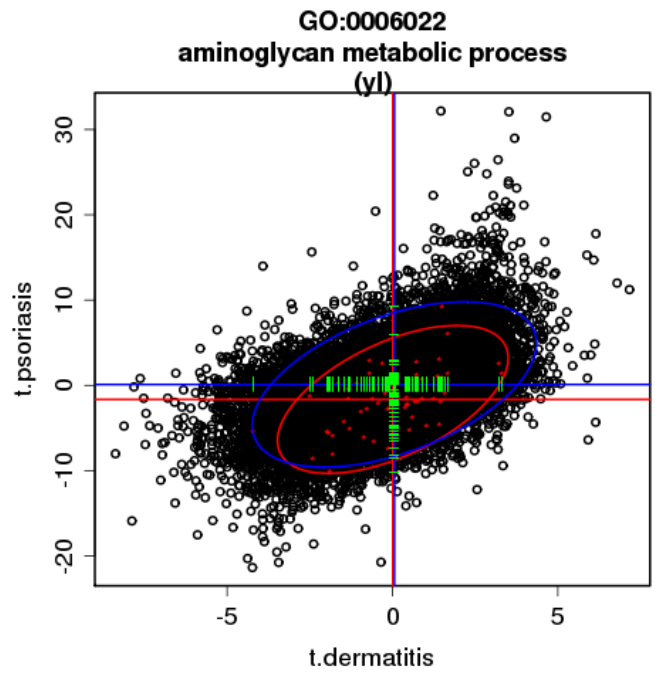
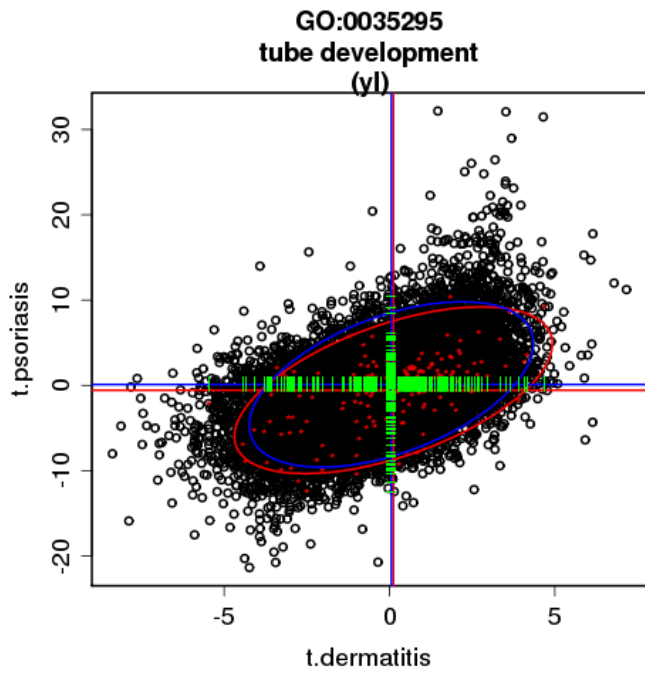


GO:0000271
polysaccharide biosynthetic process
(yl)

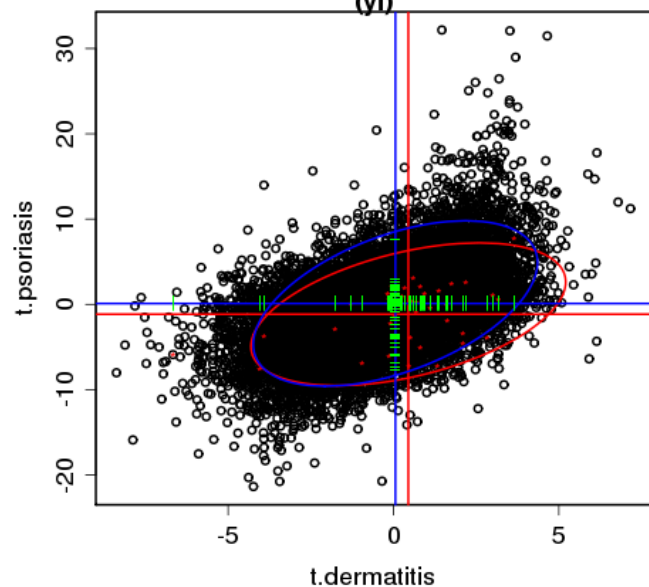




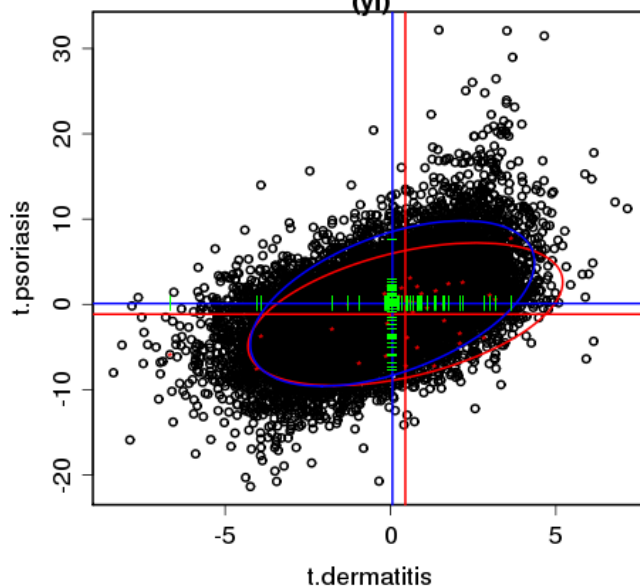




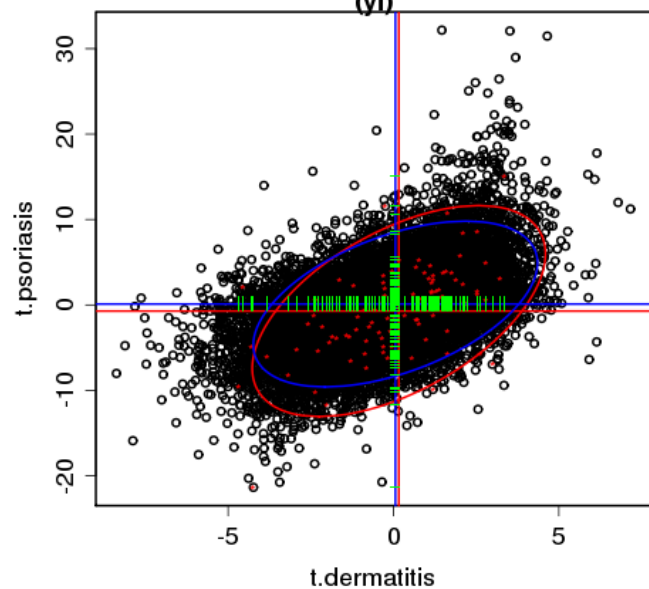
GO:0002541
activation of plasma proteins during acute inflammatory response
(yl)



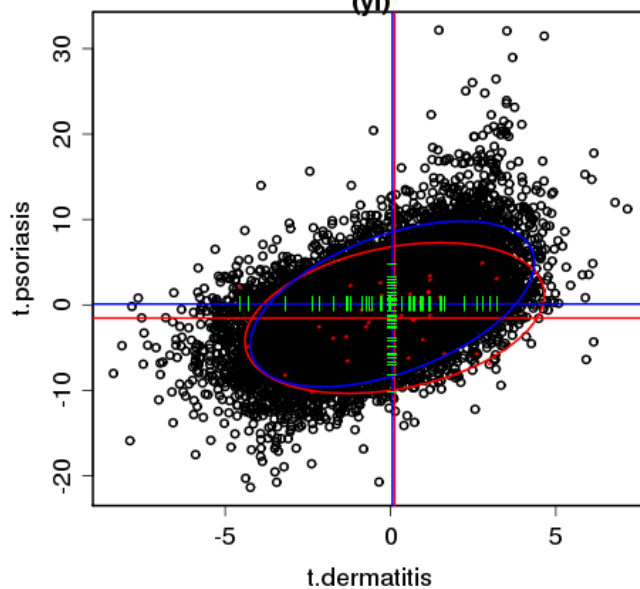
GO:0006956
complement activation
(yl)



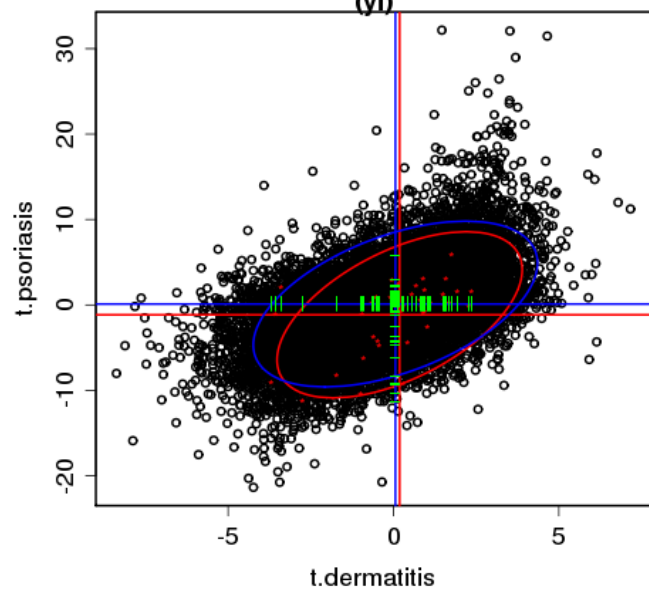
GO:0006575
amino acid derivative metabolic process
(yl)



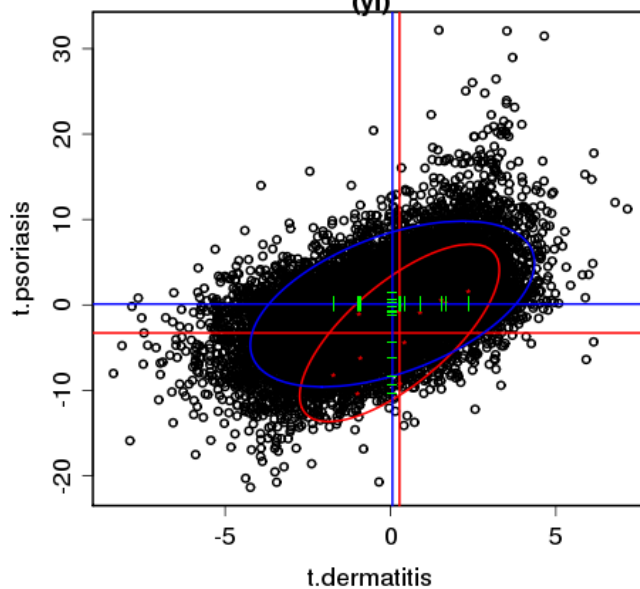
GO:0018958
phenol metabolic process
(yl)

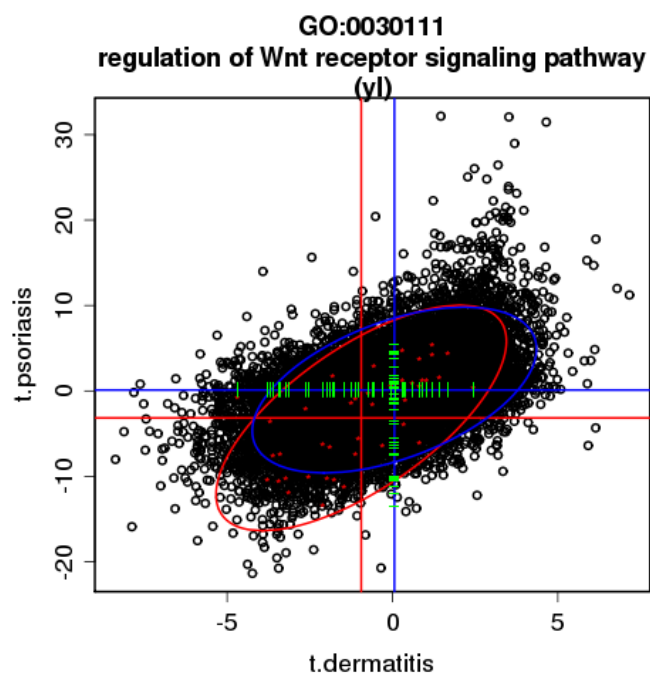
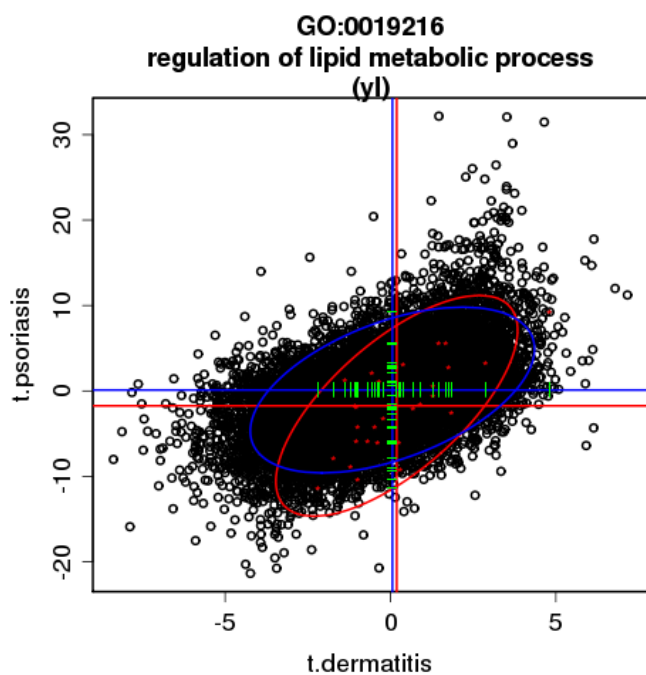
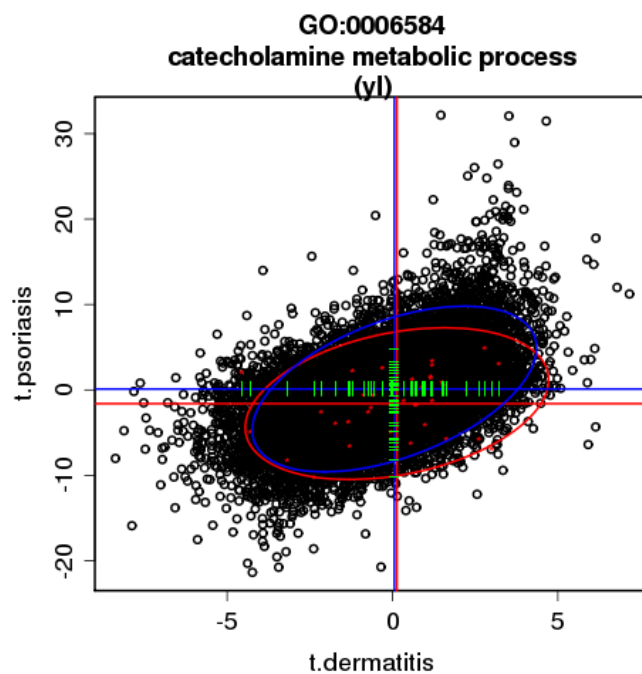
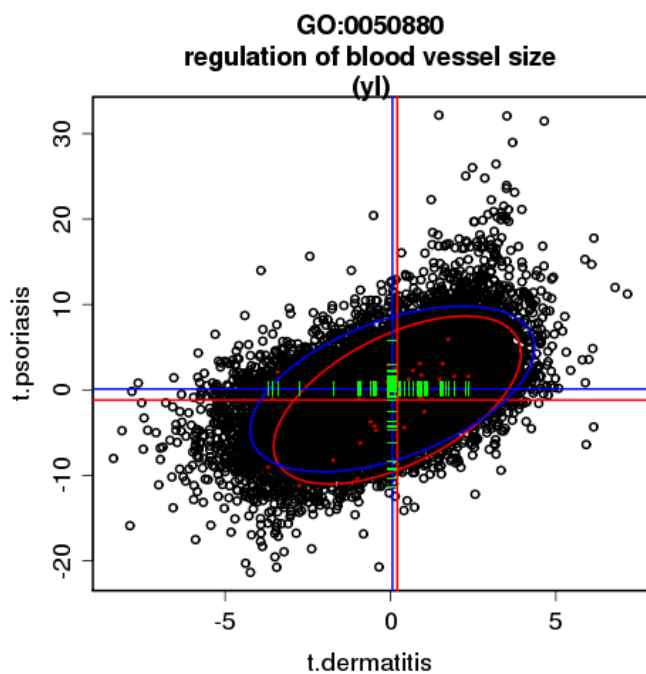
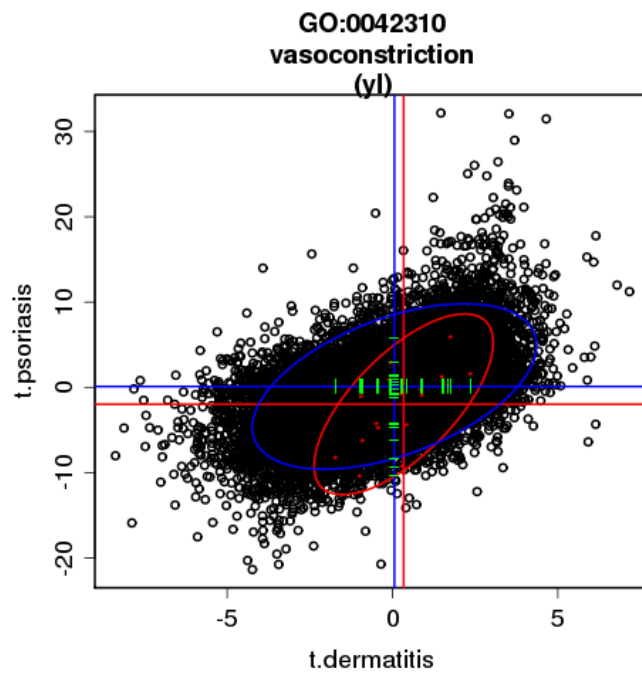
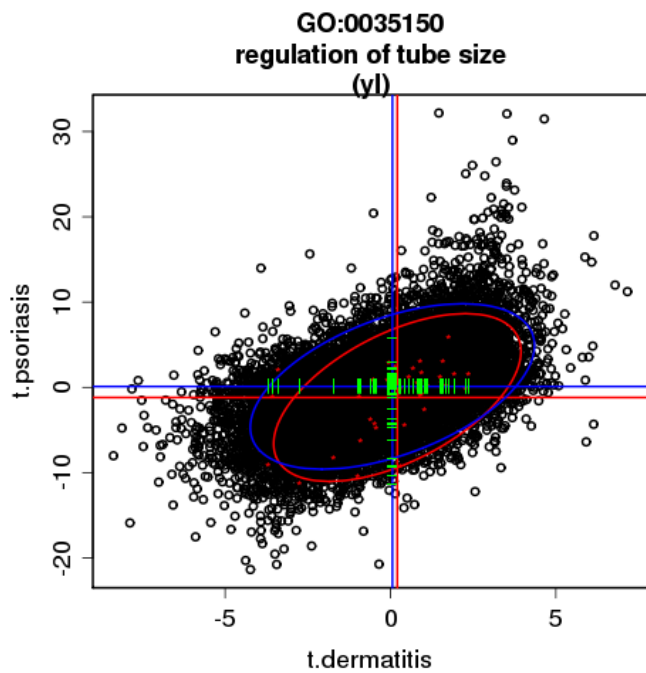


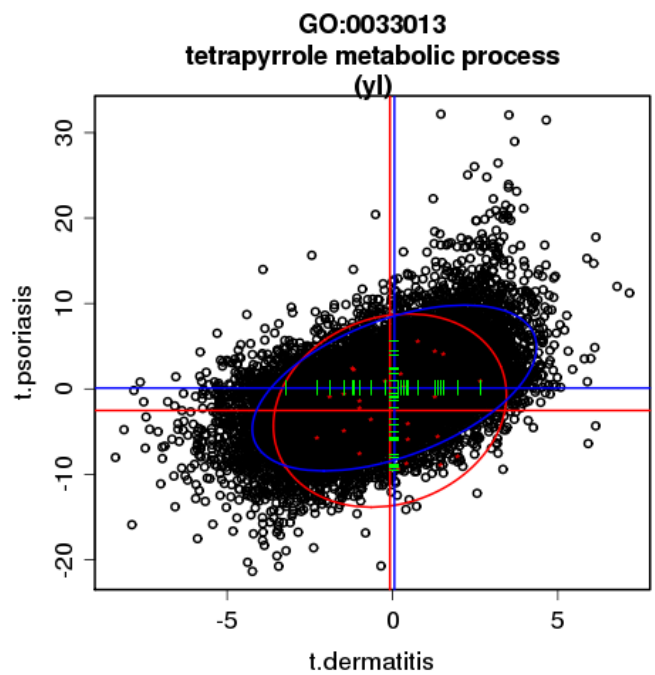
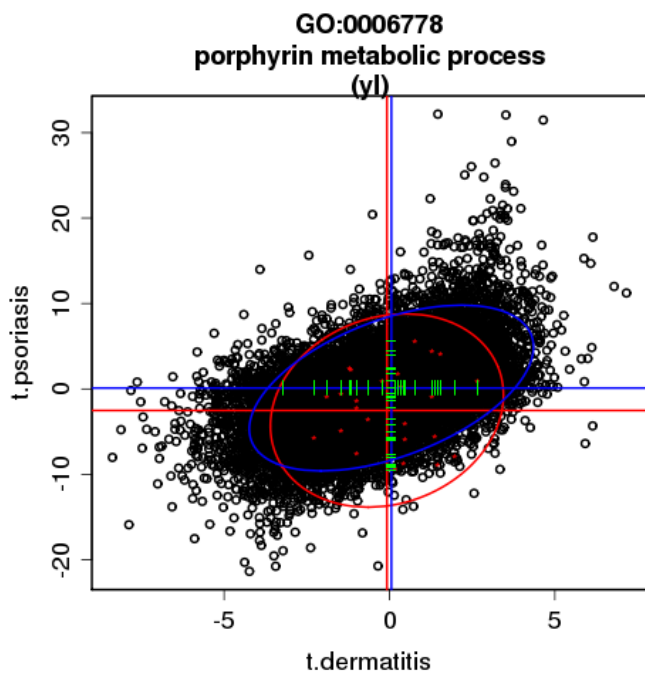
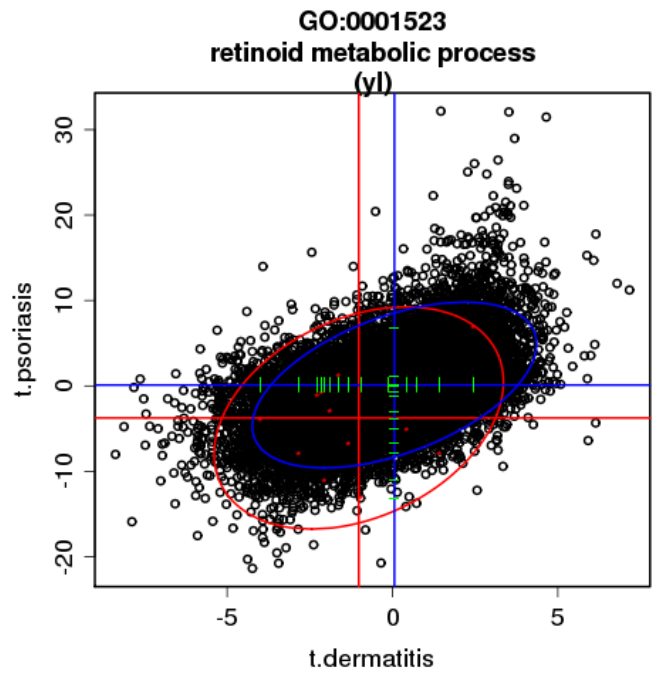
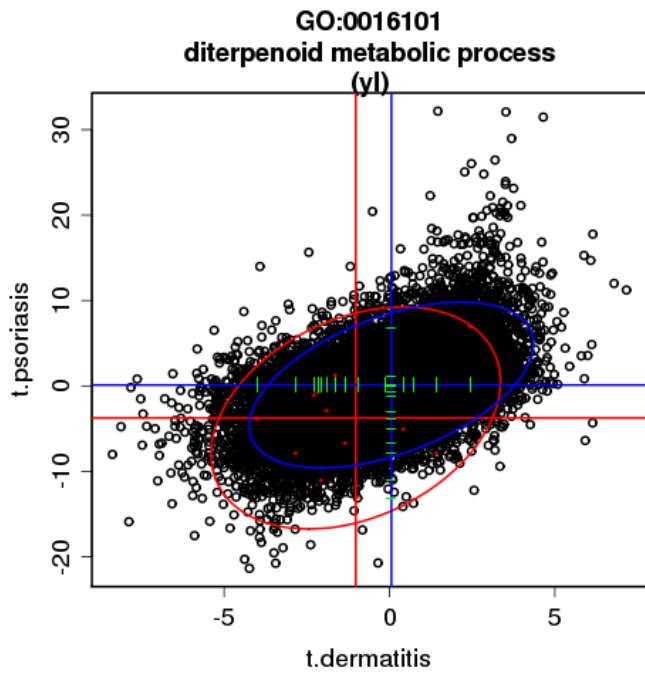
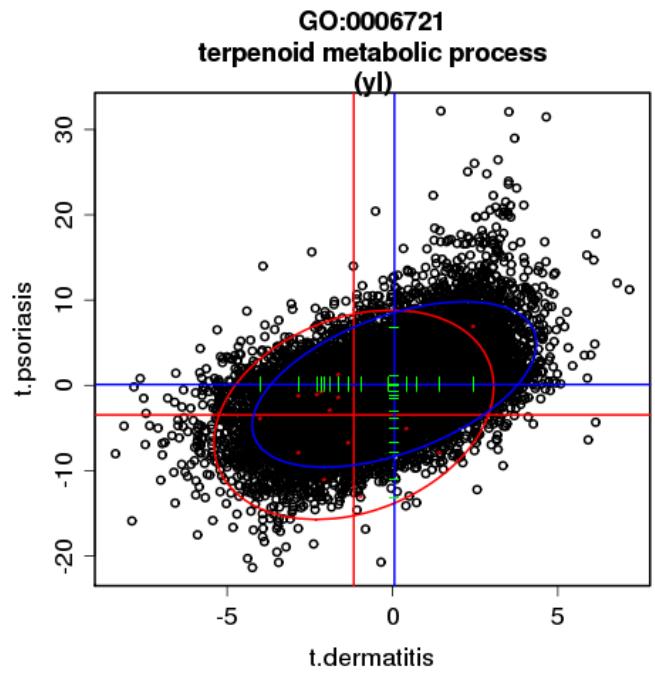
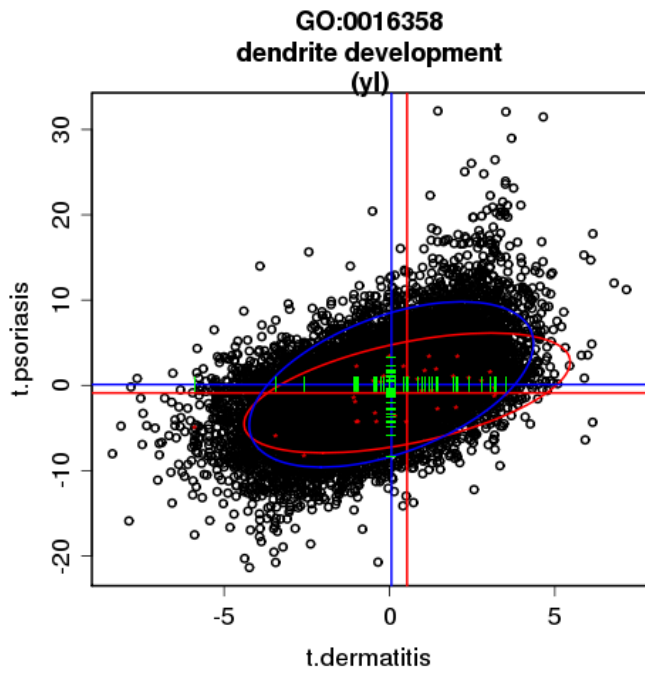
GO:0003018
vascular process in circulatory system
(yl)



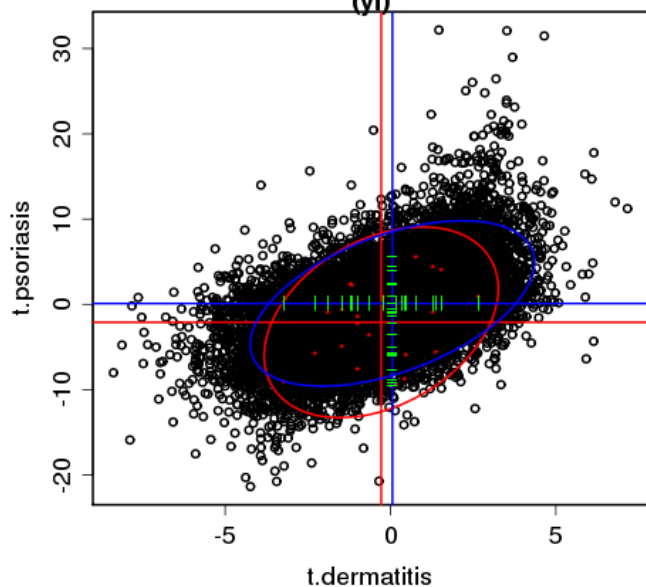
GO:0019229
regulation of vasoconstriction
(yl)



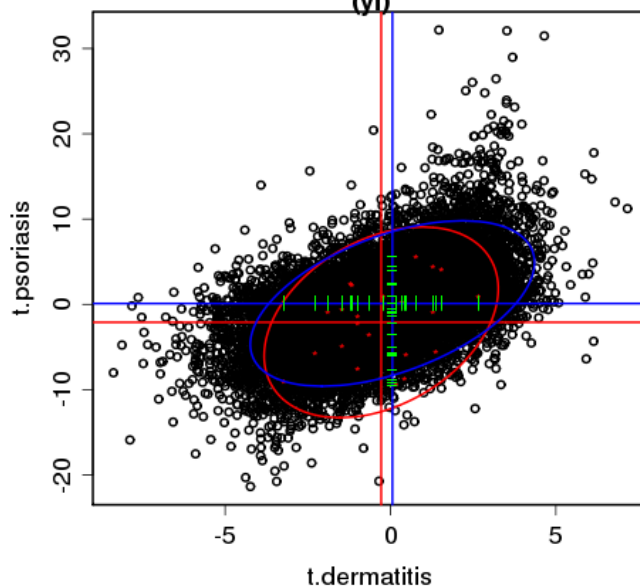




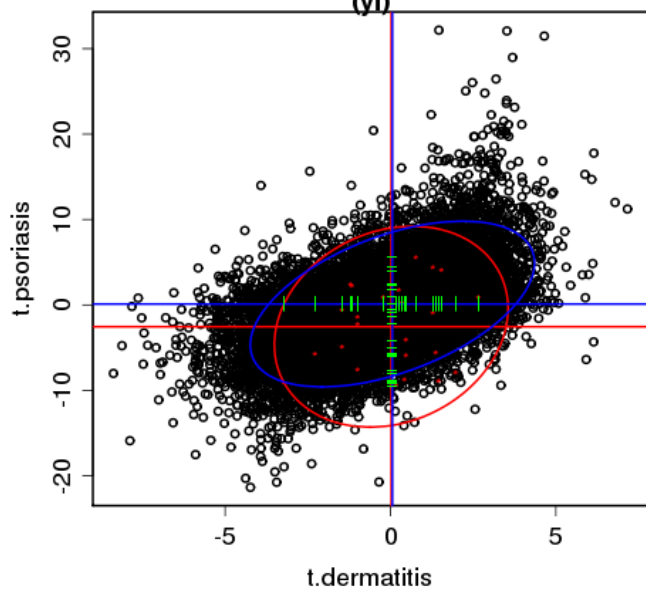
GO:0006779
porphyrin biosynthetic process
(yl)



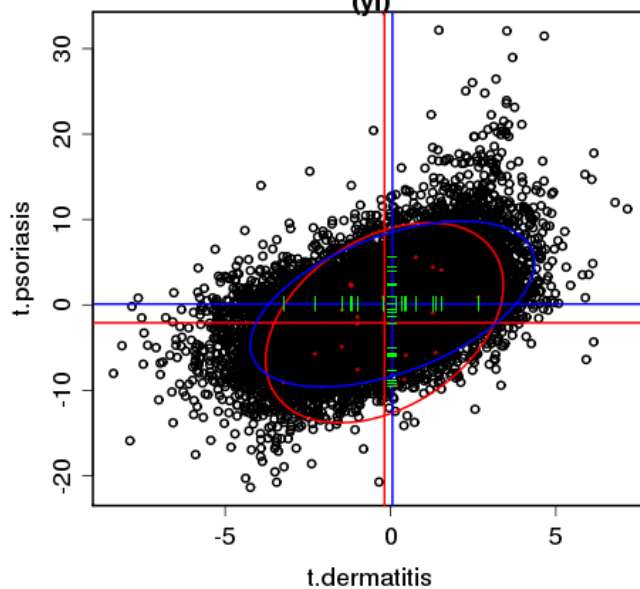
GO:0033014
tetrapyrrole biosynthetic process
(yl)



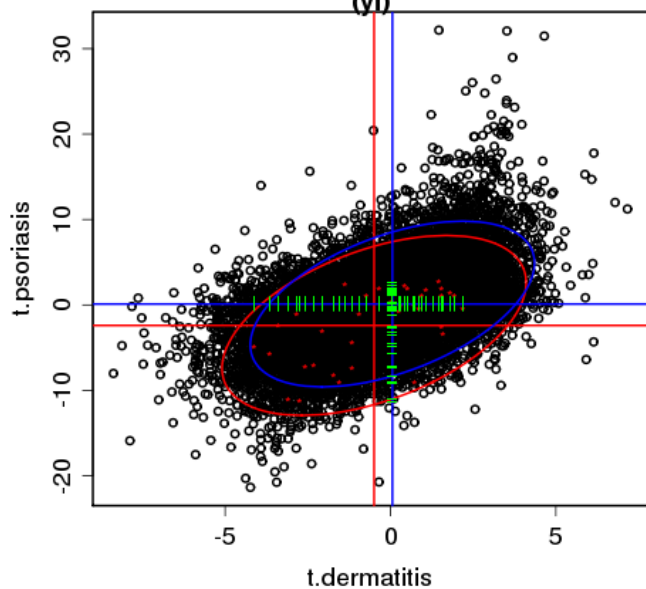
GO:0042168
heme metabolic process
(yl)



GO:0006783
heme biosynthetic process
(yl)



GO:0006937
regulation of muscle contraction
(yl)



GO:0001936
regulation of endothelial cell proliferation
(yl)

